SPECIAL POSTERS, displayed all week

Significant Improvements to the PSI Mass Special **Spectrometer Data File Standard: mzML 1.1**; <u>Matthew Chambers</u>²; Lennart Martens¹; Marc Sturm³; Darren Kessner⁴; Fredrik Levander⁵; Jim Shofstahl⁶; Wilfred Tang⁷; Angel D. Pizarro⁸; Luisa Montecchi-Palazzi¹; Natalie Tasman⁹; Mike Coleman¹⁰; Puneet Souda¹¹; Henning Hermjakob¹; Pierre-alain Binz¹²; Eric Deutsch⁹; ¹EMBL-EBI Wellcome Trust Genome Campus, Hinxton, UK; ²Vanderbilt University, Nashville, TN; ³Eberhard Karls University, Tuebingen, Germany; ⁴Cedars-Sinai Center for Applied Proteomics, Los Angeles, CA; ⁵Lund University, Lund, Sweden; ⁶Thermo Fisher Scientific, San Jose, CA; ⁷Applied Biosystems, Foster City, CA; 8University of Pennsylvania, Philadelphia, PA; ⁹Institute for Systems Biology, Seattle, WA; 10 Stowers Institute, Kansas City, MO; 11 UCLA, Los Angeles, CA; 12 Genebio - Geneva Bioinformatics, Geneva, Switzerland

Special Teaching the Masses. Development of a Mass Spectrometry Tutorial for the Biomedical Researcher; James A. Kelley¹; Josip Blonder²; Terry L. Sumpter²; Timothy D. Veenstra²; Lawrence R. Phillips¹; **National Institutes of Health, Frederick, MD; **2SAIC-Frederick, Inc., Frederick, MD

Special PSI Transitions Markup Language (TraML) for Exchange of Selected Reaction Monitoring Transition Lists; Eric Deutsch¹; Matthew Chambers²; Lennart Martens³; Brendan Maclean⁴; Jim Shofstahl⁵; Darren Kessner⁶; Fredrik Levander⁷; Pierre-Alain Binz⁸; Ruedi Aebersold^{1,9}; Mi-Youn Brusniak¹⁰; ¹Institute for Systems Biolog, Seattle, WA; ²Vanderbilt University, Nashville, TN; ³European Bioinformatics Institute, Hinxton, UK; ⁴University of Washington, Seattle, WA; ⁵Thermo Fisher Scientific, San Jose, CA; ⁶Cedars-Sinai Center for A, Los Angeles, CA; ⁷Lund University, Lund, Sweden; ⁸Genebio -Geneva Bioinformatics, Geneva, Switzerland; ⁹Swiss Federal Institute of Technology, Zurich, Switzerland; ¹⁰Institute for Systems Bio, Seattle, WA

Special Commercialization of Mass Spectrometry; Michael A. Grayson; Retired, St Charles, MO

Special ABRF 1 (Mon-Tues) PRG 2009 Study: Relative
Protein Quantification in a Clinical Matrix; Michael
J. Maccoss²; Allis S. Chien¹; David B. Friedman³; David
Hawke⁴; Jeroen Krijgsveld⁵; Kathryn S. Lilley⁶; Robert
E. Settlage⁷; Nicholas E. Sherman⁸; Chris Turck⁹;

¹Stanford University, Stanford, CA; ²University of
Washington, Seattle, WA; ³Vanderbilt University School
of Medicine, Nashville, TN; ⁴UT- M.D. Anderson Cancer
Center, Houston, TX; ⁵EMBL, Gene Expression Unit,
Heidelberg, Germany; ⁶University of Cambridge,
Cambridge, UK; ⁷Virginia Bioinformatics Institute,
Blacksburg, VA; ⁸University of Virginia, Charlottesville,
VA; ⁹Max Planck Institute, Munich, Germany

Special ABRF 2 (Wed-Thurs) PRG2009 Study: Evaluation of

ABRF 2 (Wed-Thurs) **PRG2009 Study: Evaluation of a Quantitative Proteomics Standards by Proteomics Laboratories**; <u>James Farmar</u>¹; David Arnott²; Alexander R. Ivanov³; Jeffrey A. Kowalak⁴; William S. Lane⁵; Karl Mechtler⁶; Brett Phinney⁷; Manfred R. Raida⁸; Susan T. Weintraub⁹; ¹Einstein College of Medicine, Tarrytown, NY; ²Genentech, Inc., S. San Francisco, CA; ³Harvard University HSPH, Boston, MA; ⁴NIH, Bethesda, MD; ⁵Harvard University, Cambridge, MA; ⁶IMP Research Institute of Mo, Vienna, Austria; ⁷University of CA, Davis, Davis, CA; ⁸Experimental Therapeutics Ce,

Singapore, Singapore; ⁹University of Texas HSC, San Antonio, TX

PROTEOMICS: QUANTITATION TECHNIQUES, 001-032

- MP 001 Towards Robust Quantitative MRM Plasma Analysis
 Using Nanobore Liquid Chromatography through
 Improved Nanoelectrospray Performance; Susan E.

 Abbatiello¹; Amanda Berg²; Gary Valaskovic²; Steven
 A. Carr¹; **IBroad Institute, Cambridge, MA; **2New
 Objective, Inc., Woburn, MA
- MP 002 Improved Multiple Reaction Monitoring for Targeted Quantitative Proteomics Using Dual-Stage Electrodynamic Ion Funnel Technology; <u>David T. Kaleta</u>; Errol W. Robinson; Tao Liu; Wei-Jun Qian; Rui Zhao; Jason S. Page; Keqi Tang; David G. Camp II; Richard D. Smith; *Pacific Northwest National Laboratory, Richland, WA*
- MP 003 CaptiveSpray: A New Ionization Technique to Maximizing Speed, Sensitivity, Resolution and Robustness for LCMS Protein Biomarker Quantitation; Kerry Nugent¹; Yixin Zhu¹; Peter Kent¹; Brett Phinney²; Rudy Alvarado²; ¹Michrom Bioresources, Inc., Auburn, CA; ²Univeristy of CA, Davis, Davis, CA
- MP 004 **Detection and Quantitation of Active Ricin in Food**; Sara C. Mcgrath¹; David M. Schieltz¹; Lisa G. Mcwilliams²; John R. Barr¹; ¹Centers for Disease Control and Prevention, Atlanta, GA; ²Battelle, Atlanta, GA
- MP 005 Analyzing More Than 8-Samples with iTRAQ Exploring the Changes in the Human Serum Proteome during Pregnancy; Marjan Gucek¹; Peter Scholl², Ingo Ruczinski²; John D. Groopman²; Keith P. West²; Robert N. Cole¹; ¹Johns Hopkins School of Medicine, Baltimore, MD; ²Bloomberg School of Public Health, Johns Hopkins, Baltimore, MD; ³US FDA, College Park, MD
- MP 006 Assessing the Quantitative Dynamic Range of 8-Plex iTRAQ Proteomics Reagents in Simple and Complex Mixture of Proteins; Saw Yen Ow; Malinda Salim; Phillip C Wright; The University of Sheffield, Sheffield,
- MP 007 Improved iTRAQ & TMT Quantification on an LTQ Orbitrap Equipped with a New Type of HCD Fragmentation Cell; Peter Pichler¹; Thomas Köcher²; Johann Holzmann²; Michael Schutzbier²; Goran Mitulovic³; Thomas Moehring⁴; Karl Mechtler²; Gustav Ammerer^{1,5}; ¹Christian Doppler Laboratory for Proteome Analysis, Vienna, Austria; ²IMP, Vienna, Austria; ³IMBA Inst. of Mol. Biotech., Vienna, Austria; ⁴Thermo Fisher Scientific, Bremen, Germany; ⁵University of Vienna, Vienna, Austria
- MP 008 Quantitative Proteomic Analysis and Genome
 Annotation of Candida albicans and Candida
 glabrata; Keshava T.S. Prasad¹; Kumaran Kandasamy^{1,2};
 Santosh Renuse¹; Harsh Pawar¹; Arivusudar
 Marimuthu¹; Raghothama Chaerkady^{1,2}; Pradip Kumar
 Acharya¹; Akhilesh Pandey²; ¹Institute of
 Bioinformatics,, Bangalore, India; ²Johns Hopkins
 University, Baltimore, MD
- MP 009 Cross-Sample Analysis of MRM-Based Plasma
 Protein Expression Measurements Key Component
 of Developing High Quality MRM Assays; Sean L.
 Seymour¹; Leigh Anderson²; Christie L Hunter¹;

 Applied Biosystems, Foster City, CA; ²Plasma
 Proteome Institute, Washington, DC

- MP 010 Generating Neuropeptide Standard Curve in a Single LC-MS Run by N, N-Dimethyl Amino Acids Tandem Mass Tags; Feng Xiang; Junhua Wang; Lingjun Li; University of Wisconsin, Madison, WI
- MP 011 Automated Solid Phase Sequential Isotope Labeling for Protein Quantitation; Reinout Raijmakers^{1,2}; Paul J. Boersema^{1,2}; Shabaz Mohammed^{1,2}; Albert J.R. Heck^{1,2}; ** **Utrecht University, Utrecht, Netherlands; ** **Netherlands Proteomics Centre, Utrecht, Netherlands
- MP 012 A Low Cost, Automated Chemical Derivatization Technique for Relative Proteome Quantification; Andy Lo; Joel H. Weiner; Liang Li; University of Alberta, Edmonton, Canada
- MP 013 A New Technique: Double-Stable-Isotope-Coding (DSIC) for Quantitative Proteomics; Hong Wang; Chee-Hong Wong; Alice Chin; Jacob Kennedy; Qing Zhang; Samir Hanash; PHS, Fred Hutchinson Cancer, Seattle, WA
- MP 014 Targeting and Quantifying the Hydrophobic Peptidome Fraction by High Resolution Multiple Selected Reaction Monitoring (H-mSRM); Diana Klingler²; Peter Sonderegger²; Endre Laczko¹;

 Trunctional Genomics Center ETHZ UHZ, Zurich, Switzerland; Institute of Biochemistry UZH, Zurich, Switzerland
- MP 015 Transfer of Optimized Acquisition Parameters between Mass Analyzer Types for Improved Protein Identification and Quantification; Christine Miller; David Horn; Shripad Torvi; Ning Tang; Keith Waddell; Agilent Technologies, Santa Clara, CA
- MP 016 Using High Mass Accuracy to Quantify Targeted Proteins; Amol Prakash¹; Gene Ciccimaro²; Scott Peterman²; Taha Rezai¹; Bryan Krastins¹; David Sarracino¹; Mary F Lopez¹; ¹ThermoFisher Scientific, Cambridge, MA; ²Thermo Fisher, New Jersey, NJ
- MP 017 Evaluating the Performance Factors of a Targeted Label-Free Protein Quantitation Approach on an Ultra-High Resolution API-Qq-TOF; Wolfgang Jabs; Markus Lubeck; Marina Behrens; Carsten Baessmann; Bruker Daltonik GmbH, 28359 Bremen, Germany
- MP 018 Data-Independent Tandem Mass Spectrometry
 Acquisition for Label-Free Peptide/Protein
 Quantification; Alexander Scherl¹; Jean-charles
 Sanchez¹; Judith Nicholson²; Ted Hupp²; ¹University of
 Geneva, Geneva, Switzerland; ²University of Edinburgh,
 Edinburgh, UK
- MP 019 Accurate Label-Free Quantitation of Proteins by UPLC/MSE Using Replicates; Chong-Feng Xu; Thomas A. Neubert; NYU Langone Medical Center, New York, NY
- MP 020 Unexpected Decrease of Internal Standard Signals in Quantitative MALDI-TOF Mass Spectrometry;
 Norman H.L. Chiu; Walter B. Wilson; University of North Carolina at Greensboro, Greensboro, NC
- MP 021 **Evaluation of Label-Free Relative Protein Quantification by Protein Standard Mixtures**; Andrej

 Vasilj¹; Andrej Shevchenko²; Marc Gentzel³; ¹MPI-Cell

 Biology and Genetic, Dresden, Germany; ²MP of Mol

 Cell Biology, Dresden, Germany; ³MPI-CBG, Dresden,

 Germany
- MP 022 Detection and Quantification of a Novel Plant
 Pathogen Defense Protein Mannitol Dehydrogenase
 from LC/MS^E Datasets; Kevin Blackburn; Fang-yi
 Cheng; John D. Williamson; Michael B. Goshe; NC
 State University, Raleigh, NC

- MP 023 A Label-Free Quantitation Strategy for Personalized Membrane Proteomics Signature in Colorectal Cancer; Chien-peng Wu¹; Chia-li Han¹; Chia-feng Tsai¹; Chih-wei Chien²; Pei-yi Lin¹; Guei-tian Chen³; Err-cheng Chan³; Jinn-shiun Chen⁴; Jao-song Yu³; Yu-ju Chen¹; Institute of Chemistry, Academia Sinica, Taipei, Taiwan; National Tsing Hua University, Hsin Chu, Taiwan; Chang Gung University, Tao Yuan, Taiwan; Chang Gung Memorial Hospital, Tao Yuan, Taiwan
- MP 024 BDNF-Induced Changes in the Expression of the Translation Machinery In Hippocampal Neurons: Protein Levels and Dendritic mRNA; Bruno Manadas¹; Ana Santos¹; Krisztina Szabadfi¹; João Gomes¹; Spiros D. Garbis²; Michael Fountoulakis²; Carlos B Duarte¹; ¹Center for Neuroscience and Cell Biology, Cantanhede, Portugal; ²B.R.F.A.A., Athens, Greece
- MP 025 Data-Independent Relative Quantification of Salt Stress-Induced Membrane Protein Abundance Changes in Arabidopsis thaliana Using Label-Free GeLC/MS^E.; Uma Kota; Kevin Blackburn; Steven D. Clouse; Michael B. Goshe; North Carolina State University, Raleigh, NC
- MP 026 A Rapid Label-Free Proteomics Survey of Immortalization in Cultured Human Breast Epithelial Cells; Rui Miguel Mamede Branca; Virginia Pearce; Laszlo Prokai; University of North Texas Health Science Center, Fort Worth, TX
- MP 027 Development of Robust Label-Free Proteomics for Determination of Changes in UV Induced DNA Damage.; Bei Zhao; George F. Heine; Jeffrey D. Parvin; Michael A. Freitas; Ohio State University, Columbus, OH
- MP 028 Relative Quantitation by Label-Free Techniques and Targeted Mass Spectrometry of Brain Endothelial Cell Proteins Upon Challenge with a Fungal Pathogen; Richard A. Eigenheer¹; Kiem Vu¹; Babette B. Weksler²; Angie Gelli¹; Brett S. Phinney¹; ¹UC Davis, Davis, CA; ²Cornell University, Ithica, NY
- MP 029 Validation of RNAi Protein Knockdown Using
 Targeted Proteomics; Daniela Tomazela; Gennifer
 Merrihew; Geoff Findlay; Veronika Glukhova; Frances
 Mao; Willie Swanson; Ray Monnat Jr; Michael J.
 Maccoss; University of Washington, Seattle, WA
- MP 030 Monitoring Proteomes of Transgenic Peanuts
 Engineered for Reduced Allergen Content by Using
 Linear Trap Quadrupole and Triple Quadrupole
 Mass Spectrometry; Severin E. Stevenson¹; Ye Chu²;
 Peggy Ozias-Akins²; Jay J. Thelen¹; JUM BiochemProteomics, Columbia, MO; ²University of GeorgiaTifton, Tifton, GA
- MP 031 GeLC-Multiple Reaction Monitoring Mass
 Spectrometry of Membrane Expression of Cystic
 Fibrosis Transmembrane Conductance Regulator;
 Alexis Ramos; Hui Jiang; Xudong Yao; Department of
 Chemistry, University of Connecticut, Storrs, CT
- MP 032 Identification of Biomarkers for Diabetic
 Retinopathy by Multiple Reaction Monitoring;
 Kyunggon Kim¹; Jiyoung Yu¹; Kyong Soo Park²;
 Hyeong Gon Yu³; In-Jin Jang⁴; <u>Youngsoo Kim</u>¹; <u>Ipept.</u>
 of Biomedical Sciences, College of Medicine, Seoul Nat'l
 Univ, Seoul, South Korea; <u>Ipept.</u> of Internal Medicine,
 College of Medicine, Seoul Nat'l Univ, Seoul, South
 Korea; <u>Ipept.</u> of Ophthalmology, College of Medicine,
 Seoul Nat'l Univ, Seoul, South Korea; <u>Ipept.</u> of

Pharmacology, College of Medicine, Seoul Nat'l Univ, Seoul, South Korea

BIOINFORMATICS: QUANTITATION, 033 - 065

- MP 033 **Quantitative Analysis Methods in Proteomics**; Ashoka D. Polpitiya; Weijun Qian; Vladislav A Petyuk; Gordon Anderson; Richard D. Smith; *Pacific Northwest National Lab, Richland, WA*
- MP 034 Automatic Computational Protein Co-Regulation Screening for Quantitative Mass Spectrometry Experiments; Marc Kirchner^{1,2}; Bernhard Y Renard^{2,3}; Ullrich Koethe²; Judith AJ Steen¹; Hanno Steen¹; Fred A Hamprecht^{2,3}; Harvard Medical School / Children's Hospital, Boston, MA; ²University of Heidelberg, Heidelberg, Germany; ³Children's Hospital Boston, Boston, MA
- MP 035 Shared Peptides in Mass Spectrometry Based Protein Quantification; Banu Dost¹; Nuno Bandeira²; Vineet Bafna³; ¹University of California, San Diego, La Jolla, CA; ²University of California,, La Jolla, CA; ³Univ. Cal. San Diego, San Diego, CA
- MP 036 Identifying and Quantifying Isoforms and Homologues; Johannes PC Vissers¹; Richard R Sprenger²; Lennart Martens³; Scott Geromanos¹; Jim Langridge¹; ¹Waters Corporation, Manchester, UK; ²Department of Medical Biochemistry, AMC, Amsterdam, Netherlands; ³EMBL European Bioinformatics Institute, Hinxton, UK
- MP 037 Automated, XIC Based Protein Quantitation of Comparative Low-Resolution 2D/LC Shotgun Experiments within the Elucidator System.; Eberhard Durr¹; Peter Askovich²; Lori C Stansberry¹; Mark A Miller¹; Loren D Schultz¹; Joseph G Joyce¹; ¹Merck & Co, West Point, PA; ²2 Rosetta Biosoftware, Seattle, WA
- MP 038 Mathematical Modelling of Dynamic Exclusion to Optimize Protein and Spectral Counts in MudPIT;

 Ying Zhang; Zhihui Wen; Laurence Florens; Michael Washburn; Stowers Institute for Medical Research, Kansas City, MO
- MP 039 Algorithms for Label-Free Protein Quantification Across Hundreds of LC-MS Data Sets; Zia Khan; Joshua Bloom; Benjamin Garcia; Mona Singh; Leonid Kruglyak; Princeton University, Princeton, NJ
- MP 040 Assessing Reproducibility of Label-Free Proteomics Platforms Using a Large Rat Sera Study: A Comparison of Microspray and Nanospray; Xiaofeng Guo¹; Vasant Marur¹; Neil Russell¹; Matthew J Sniatynski¹; Michael Anthanas²; Bruce Kristal^{1,3};

 ¹Brigham and Women's Hospital, Boston, MA; ²VAST Scientific, Cambridge, MA; ³Harvard Medical School, Boston, MA
- MP 041 Evaluation of Label Free Differential Mass
 Spectrometry to Detect Low Level Proteins in
 Unfractionated Complex Mixture; Sheeno
 Thyparambil; Shweta S Chavan; Veronica MacLeod;
 Rick Edmondson; Univ Arkansas Med Sci., Little Rock,
 AR
- MP 042 **Peptide Normalization Increases Sensitivity of Label- Free Quantification of Proteins**; <u>Richard LeDuc</u>;

 Jeffery Hiken; Henry W. Rohrs; Monica Bessler; R.
 Reid Townsend; *Washington University, St. Louis, MO*
- MP 043 New Algorithm for Label-Free Protein
 Quantification; Weiwu Chen¹; Baozhen Shan¹; Eric
 Bonneil²; Janine Voyer¹; Gilles Lajoie³; Pierre Thibault²;
 Bin Ma⁴; ¹Bioinformatics Solutions Inc., Waterloo, ON;
 ²Univ.of Montreal, Montreal, QC; ³University of Western

- Ontario, London, ON; ⁴University of Waterloo, Waterloo, Canada
- MP 044 Novel Label-Free Quantitation Algorithms to Analyze Large Numbers of Proteome/Metabolome Samples; Ken Aoshima^{1,2}; Satoshi Tanaka^{1,2}; Tatsuji Nakamura^{1,2}; Hideki Watanabe¹; Khin Than Myint^{1,2}; Junro Kuromitsu¹; Yoshiya Oda^{1,2}; ¹Eisai Co., Ltd, Ibaraki, Japan; ²CREST, Saitama, Japan
- MP 045 **Evaluation of Relative Quantitation in Proteomics with Label-Free Methods**; Bernd Roschitzki^{1,2}; <u>Bertan</u>
 <u>Gerrits</u>²; Christian Panse^{2,}; Jonas Grossmann^{2,}; Simon
 Barkow-Oesterreicher^{2,}; Ralph Schlapbach²; ¹University
 of Zurich, Zurich, Switzerland; ²ETH Zurich FGCZ,
 Zurich, Switzerland
- MP 046 Label Free Proteomics: Utilizing the Computational Proteomic Analysis System for Relative Protein Quantitation; Lewis C Jackson; Mark Lovell; Bert C. Lynn; University of Kentucky, Lexington, KY
- MP 047 Identification Of Mosquito Salivary Gland Proteins and Determination of Parasite Infection; Marcus Macht¹; Aditya P. Dash²; Hebeler Romano¹; Arun Sharma²; **IBruker Daltonics GmbH, Bremen, Germany; **National Institute for Malaria Research, New Delhi, India
- MP 048 Label-Free Differential Analysis: An Iterative Approach to Increased Coverage, Improved Statistics and Results; Michael Athanas¹; Michael J. Maccoss²; Amol Prakash³; Lukas Kall²; Daniela Tomazela²; Brendan Maclean²; Taha Rezai³; Bryan Krastins³; David Sarracino³; Scott Peterman⁴; Mary F Lopez³; ¹VAST Scientific, Cambridge, MA; ²University of Washington, Seattle, WA; ³ThermoFisher Scientific, Cambridge, MA; ⁴ThermoFisher Scientific, Somerset, NJ
- MP 049 Comparative Analysis of Paired Samples from Distinct Proteomics Mixtures Using CRAWDAD;

 Eric Rynes¹; Greg L. Finney¹; Daniela Tomazela¹; F. Sessions Cole²; Aaron Hamvas²; Michael J. MacCoss¹;

 Dept. of Genome Sciences, University of Washington, Seattle, WA; ²Dept. of Pediatrics, Washington University, St. Louis, MO
- MP 050 Utilization of High-Accuracy FTICR-MS Data in Protein Quantitation Experiments; Martin Strohalm^{1,2}; Petr Novak¹; Petr Pompach¹; Petr Man¹; Daniel Kavan¹; Matthias Witt³; Pert Dzubak⁴; Marian Hajduch⁴; Vladimir Havlicek^{1,4}; Institute of Microbiology, Prague, Czech Republic; Institute of Chemical Technology, Prague, Czech Republic; Bruker Daltonik GmbH, Bremen, Germany; Palacky University, Olomouc, Czech Republic
- MP 051 MassComp-Q: A Comprehensive Quantitation
 Software Tool for Stable Isotope Labeling and LabelFree Quantitative Proteomics; Chih-Chiang Tsou;
 Ting-Yi Sung; Wen-Lian Hsu; Institute of Information
 Science, Academia Sinica, Taipei, Taiwan
- MP 052 A Computational Method for Improved Quantitation Accuracy of Differentially 18O/16O Labeled Peptides Exhibiting Variable Rate of 18O Incorporation;

 Xiaoying Ye¹; Brian Luke¹; Donald Johann²; Thorkell Andresson¹; Timothy D. Veenstra¹; Josip Blonder¹;

 ISAIC-Frederick Inc., Frederick, MD; ²NIH, Bethesda, MD
- MP 053 Quantitative Approach to Proteome Analysis of Human Body Fluids Based on AMT Tags and Isotopic Labeling; Igor Popov^{1,2}; Ilya A Agron^{2,3}; Alexey Kononikhin²; Dmitry Avtonomov^{2,3}; Oxana Trifonova⁴; Irina Larina⁴; Eugene Nikolaev^{1,2}, Institute

- for Energy Problems of Chemical Physics, Moscow, Russia; ²Emanuel Institute of Biochemical Physics RAS, Moscow, Russia; ³Ins. for Biomedical Chem. Rus. Acad. Med.Sciences, Moscow, Russia; ⁴Institute for Biomedical Problems RAS, Moscow, Russia
- MP 054 Algorithm for Quantification of Stable Isotope
 Labeled Peptides; Yingxin Zhao; Sigmund Haidecher;
 Ronald Tilton; Larry Denner; Jonathan Starkey;
 Rovshan Sadygov; University of Texas, Galveston, TX
- MP 055 High-Throughput Measurement of Protein Turnover in Plants Using Stable Isotope Labeling Coupled with LC-MS/MS Analysis; Wen-Ping Chen¹; Xiao-Yuan Yang^{1,4}; Adrian D. Hegeman^{1,4}; Aaron K. Rendahl²; Sanford Weisberg²; Thomas F. McGowan³; William M. Gray⁴; Jerry D. Cohen¹; ¹Dept. Horticultural Science -U of MN, Saint Paul, MN; ²School of Statistics U of MN, Saint Paul, MN; ³Center for Mass Spectrometry and Proteomics U of MN, Saint Paul, MN; ⁴Dept. Plant Biology U of Minnesota, Saint Paul, MN
- MP 056

 SILAC Quantification with PEAKS to a Depth of 3000 Proteins from a Double Knockout GSK-3 of Mouse Embryonic Stem Cells; Chris Hughes¹; Brad Doble³; Lei Xin²; Clark Chen²; Baozhen Shan²; Bin Ma⁴; Gilles Lajoie¹; ¹University of Western Ontario, London, ON; ²Bioinformatic Solutions Inc., Waterloo, ON; ³McMaster University, Hamilton, ON; ⁴University of Waterloo, Waterloo, ON
- MP 057 **Automatic Quantification of 16/18O Labeled LC/MS Data;** Anna Kreshuk¹; Marc Kirchner¹; Bernhard Y.

 Renard¹; Dominic Winter²; Hanno Steen³; Judith A. J.

 Steen³; Wolf D. Lehmann²; Fred A. Hamprecht¹;

 ¹University of Heidelberg, Heidelberg, Germany;

 ²German Cancer Research Center, Heidelberg,

 Germany; ³Harvard Medical School/Children's Hospital

 Boston, Boston, MA
- MP 058 Quantitation across Multiple iTRAQ Samples Using Scaffold Q+; Charles E Roberts¹; Jason Nunes¹; Brian C. Searle¹; **IProteome Software, Portland, OR
- MP 059 Mathematical Modeling and Assessment of
 Quantitation Following Abundant Protein Depletion
 Using Hexapeptide Beads and iTRAQ; John H.
 Schwacke; Lashanda Waller; Daniel R. Knapp; Medical
 University of South Carolina, Charleston, SC
- MP 060 Improved Technique for Automated Analysis of iTRAQ Data Using LTQ-Orbitrap; Getiria I.

 Onsongo; Susan K. Van Riper; Kofi P. Adragni; Ebbing De Jong; Matthew D. Stone; Sricharan Bandhakavi; Baolin Wu; John V. Carlis; Timothy J. Griffin; University of Minnesota, Minneapolis, MN
- MP 061 A Bioinformatic Tool for Detailed Interrogation of
 Multiple iTRAQ Datasets; Erika P Parkinson¹; Andrew
 Garrow²; Paul J Skipp¹; Maja Aleksic²; Andrew White²;
 Geraldine Clough¹; Daniel J Scott²; C. David O'Connor¹;

 ¹University of Southampton, Southampton, UK; ²Safety
 & Environmental Assurance Centre, Unilever,
 Sharnbrook, UK
- MP 062 **Templated Proteogenomics: A Novel Method for Monoclonal Antibody Sequencing**; Natalie E

 <u>Castellana</u>¹; Victoria Pham²; David Arnott²; Jennie Lill²; Vineet Bafna¹; ¹UCSD, La Jolla, CA; ²Genentech, Inc., S. San Francisco, CA
- MP 063 Development of a Reliable and Efficient Genome Annotation Pipeline Using Proteomic Mass Spectrometry Data; Markus Brosch; Tim Hubbard; Jyoti Choudhary; Wellcome Trust Sanger Instit, Cambridge, UK

- MP 064 Assigning Proteins Identified from Tissues to Cells
 Using Publicly Available Gene Chip Data; Kenneth
 Parker; BG-Medicine, Waltham, MA
- MP 065 Formulation of a MySQL Database and Query
 Toolset to Extract Complex Metabolic Information
 from a Natural Microbial Consortia.; Nathan C.
 Verberkmoes¹; Brian Dill¹; Brian Thomas²; Denise
 Schmoyer¹; Manesh Shah¹; Vincent Denef²; Paul
 Wilmes²; Patricia Carey¹; Steve Singer³; Korin
 Wheeler³; Michael Thelen³; Robert Hettich¹; ¹Oak Ridge
 National Lab, Oak Ridge, TN; ²University of California,
 Berkeley, Berkeley, CA; ³Lawrence Livermore National
 Laboratory, Livermore, CA

PROTEOMICS: BIOMARKER DISCOVERY, 066 - 097

- MP 066 Markers of Ovarian Endometrioid Cancer Using a
 Genetically Engineered Mouse Model and Pathway
 Analysis; David M. Lubman; Hyeyeung Kim; Rong Wu;
 Kathleen Cho; David Misek; University of Michigan,
 Ann Arbor, MI
- MP 067 Protein Composition of Liver Cyst Fluid from the BALB/c-cpk/+ Mouse Model of Autosomal Recessive Polycystic Kidney Disease (ARPKD); Xianyin Lai¹; Bonnie L. Blazer-Yost^{1,2}; Vincent H. Gattone II¹; Monalisa N. Muchatuta²; Frank A. Witzmann¹; Indiana University School of Medicine, Indianapolis, IN; Indiana University Purdue University at Indianapolis, Indianapolis, IN
- MP 068 Proteomic Analysis of Differentiation Factors:
 Retinal Ganglion Cell Line Differentiated by CoCulture with Non-Pigmented Ciliary Epithelium Cell
 Secreted Proteins; Ming-Hui Yang¹; Shiang-Bin Jong²;
 Jen-Taie Shiea¹; Yu-Chang Tyan²; National Sun YatSen Univ., Kaohsiung, Taiwan; Kaohsiung Medical
 University, Kaohsiung, Taiwan
- MP 069 **Biomarker Discovery by Stable Isotope Labeling of**Mouse Models; Michaela D Filiou; Yaoyang Zhang;
 Birgit Bisle; Elisabeth Frank; Melanie S Kessler; Boris
 Hambsch; Stefan Reckow; Katrin Haegler; Giuseppina
 Maccarrone; Rainer Landgraf; Christoph W Turck; Max
 Planck Institute of Psychiatry, Munich, Germany
- MP 070 Identification of Novel Urinary Biomarkers of Renal Obstruction Using Temporal Quantitative Proteomics; Ali R. Vaezzadeh^{1,2}; Andrew Briscoe²; Lee Dicker³; Oliver Hoffman³; Winston Hyde³; Hanno Steen^{1,2}; Richard S. Lee^{1,2}; Harvard Medical School, Boston, MA; ²Children's Hospital Boston, Boston, MA; ³Harvard School of Public Health, Boston, MA
- MP 071 **Label-Free Quantitative Studies of Pancreatic**Cancer Stem Cells; Lan Dai¹; David M. Lubman¹;

 ¹University of Michigan, Ann Arbor, MI
- MP 072 Proteomic analysis of Tumor Necrosis Factor-Alpha Resistant Human Breast Cancer Cells Reveals a MEK5/Erk5-Mediated Epithelial-Mesenchymal Transition Phenotype; Changhua Zhou¹; Ashley Nitchke²; Wei Xiong²; Qiang Zhang¹; Yan Tang²; Michael Bloch²; Steven Elliott²; Yun Zhu²; Lindsey Bazzone²; David Yu²; Christopher B. Weldon²; John A. McLachlan²; Rachel Schiff²; Babara S. Beckman²; Thomas Wiese¹; Kenneth P. Nephew²; Bin Shan²; Matthew Burow²; Guangdi Wang¹; ¹Xavier University of Louisiana, New Orleans, LA; ²Tulane University School of Medicine, New Orleans, LA
- MP 073 Withdrawn
- MP 074 Comparative Proteomic Analysis of Liver Cancer Stem Cells; Sheng-Ta Tsai¹; Chia-Ning Shen¹; Chih-Chiang Tsou²; Wan-Yu Mao¹; Wei-Chao Chang¹; Wen-

_	MONDAY	POSTERS	•
MP 075	Lian Hsu ² ; Chung-Hsuan Chen ¹ ; ¹ Genomics Research Center, Academia Sinica, Taipei, Taiwan; ² Institute of Information Science, Academia Sinica, Taipei, Taiwan Determining the Origin of Estradiol-Reactive Vitelline Envelope Protein Fragments in Female Rainbow Trout Using MALDI-TOF-MS and MS/MS;	MP 086	Lubman ¹ ; ¹ University of Michigan, Ann Arbor, MI; ² University of Florida, Jacksonville, FL Identification of Differentially Spiked Proteins from Un-Depleted and Un-Fractionated Human Plasma; Jose E. Meza ¹ ; Steven C. Hall ² ; H. Ewa Witkowska ² ; Susan J. Fisher ² ; ¹ Agilent Technologies, Santa Clara,
MP 076	Kimberly Salinas ¹ ; Sherry Vickery ¹ ; Candice Lavelle ² ; Michael Hemmer ¹ ; ¹ U.S. EPA, Gulf Breeze, FL; ² U.S. EPA-Student Services Contractor, Gulf Breeze, FL Analysis of Synovial Lavage and Plasma from Identical Twins to Identify Osteoarthritis	MP 087	CA; ² UCSF MS Core Facility, San Francisco, CA Serum Biomarker Discovery of Alzheimer-Related Peptides in Presymptomatic Patients by Means of 2D Protein and Peptide Separation on Monolithic Columns; Linda IJsselstijn ¹ ; Deborah Kronenberg ¹ ;
	Biomarkers; Haihong Zhou ¹ ; Joseph Menetski ¹ ; Hua Lin ² ; Shanhua Lin ² ; Christopher Becker ² ; Xuemei Zhao ¹ ; Stephen Oakley ³ ; Tim Spector ³ ; Suzanne Mandala ¹ ; Ronald Hendrickson ¹ ; ¹ Merck & Co., Inc., Rahway, NJ; ² PPD Biomarker Discovery Sciences, Menlo Park, CA; ³ St. Thomas' Hospital, King's College	MP 088	Remco Swart ² ; Peter J. Koudstaal ¹ ; Peter A. E. Sillevis Smitt ¹ ; Monique M. B. Breteler ¹ ; Theo M. Luider ¹ ; ¹ Erasmus University Medical Center, Rotterdam, The Netherlands; ² Dionex Benelux B.V., Amsterdam, The Netherlands Discovery of Novel Colorectal Cancer Biomarkers in
MP 077	London, London, UK Urinary Biomarker for Benign Prostatic Hyperplasia - Discovery Using MALDI-TOF-Based Biostatistics Combined with LC-ESI/MS/MS-Based Stable- Isotope Labeling; Shu-Hui Chen ¹ ; Hong-Lin Cheng ¹ ; Bing-Yuan Ou ¹ ; Hung-Jen Huang ¹ ; Nan-Haw Chow ¹ ; Yen-Wen Chen ² ; National Cheng Kung University, Tainan, Taiwan; National Central University, Chuang-		Dissected Colorectal Epithelia and their targeted Verification in Plasma.; Silvia Surinova ¹ ; Marta Dziechciarková ² ; Andreas Panagiotidis ¹ ; Matej Skrovina ³ ; Bruno Domon ¹ ; Marián Hajdúch ² ; Ruedi Aebersold ^{1,4} ; Institute of Molecular Systems Biology (ETHZ), Zurich, Switzerland; ² Palacký University and University Hospital, Olomouc, Czech Republic; ³ J.G.Mendel Oncology Centre, Novy Jicin, Czech
MP 078	Li, Taiwan Proteomic Analysis to Understanding a Retinoid- Hypersensitive Embryonal Carcinoma Cell Mutant; Qishan Lin; Jinghua Zhu; Paulette McCormick; University at Albany, Rensselaer, NY	MP 089	Republic; ⁴ Institute for Systems Biology, Seattle, WA Multiplex Longitudinal Proteomic Profiling of Human Sera in the Study of the Pathogenesis of Type-1 Diabetes; Robert Moulder ¹ ; Waltteri Hosia ² ; Olli Simell ³ ; Riitta Lahesmaa ¹ ; ¹ Turku Centre for
MP 079	Systematic Evaluation of Immobilized pH Gradient- Isoelectric Focusing (IPG-IEF) for Salivary Biomarker Discovery; Jonathan L. Bundy ¹ ; Michael Gardner ¹ ; Megan Rowland ² ; James Stephenson ¹ ;	MP 090	Biotechnology, Turku, Finland; ² Karolinska Institute, Stockholm, Sweden; ³ Faculty of Medicine, University of Turku, Turku, Finland Differential Proteome Profiling Using iTRAQ in
MP 080	Research Triangle Institute, Rtp, NC; ² RTI International, Cary, NC Comparison of Ultrastructure and Protein Composition of Planktonic and Biofilm Stages of Non-Typeable Haemophilus Influenzae; James Kerwin; Siva Wu; Paul Webster; House Ear Institute, Los Angeles, CA		Microalbuminuric and Normoalbuminuric Type 2 Diabetic Patients; Hopil Min ¹ ; Yeonjung Kim ¹ ; Yunhyi Ku ² ; Ji Yoon Lee ³ ; Kyong Soo Park ² ; Youngsoo Kim ¹ ; ¹ Dept. of Biomedical Sciences, College of Medicine, Seoul Nat'l Univ, Seoul, South Korea; ² Dept. of Internal Medicine, College of Medicine, Seoul Nat'l Univ, Seoul, South Korea; ³ National Instrumentation Center for
MP 081	Comparison of Tumour and Normal Endometrial Samples by LC-MS/MS Using an Iterative Exclusion List Approach; Sebastien Voisin ¹ ; Leroi Desouza ¹ ; Olga Krakovska ¹ ; Alexander D. Romaschin ² ; Terence J Colgan ³ ; K W Michael Siu ¹ ; ¹ York University, Toronto, Canada; ² St Michael's Hospital, Toronto, Canada; ³ Mt Sinai Hospital, Toronto, Canada	MP 091	Environmental, Seoul Nat'l Univ, Seoul, South Korea Profiling the Post-Translational Modifications of Human Serum Albumin; Christine Jelinek ¹ ; Rebekah Gundry ² ; Jessica E. Mott ¹ ; Robert O'meally ¹ ; Jennifer Van Eyk ² ; Robert J. Cotter ¹ ; ¹ Johns Hopkins School of Medicine, Baltimore, MD; ² Johns Hopkins University, Baltimore, MD
MP 082	Urinary Glycoprotein Biomarker Discovery for Human Bladder Cancer Using Multi-Lectin Affinity Chromatography and LC-MS/MS; Na Yang ¹ ; Shun Feng ¹ ; Huy Vuong ¹ ; Steve Goodison ² ; Charles J. Rosser ² ; Fan Xiang ³ ; David M. Lubman ¹ ; ¹ University of Michigan, Ann Arbor, MI; ² University of Florida, Jacksonville, FL; ³ Shimadzu Biotech, Pleasanton, CA	MP 092	Identification of <i>in vitro</i> Modified Lipoproteins Using MALDI Tandem Mass Spectrometry and a Reduced Proteins Database Approach.; Omar Belgacem ¹ ; Helen Montgomery ² ; Matthew Openshaw ¹ ; Wu Zidian ¹ ; Sobal Grazyna ³ ; Gerald Stubiger ⁴ ; Ishimadzu Biotech, Manchester, UK; Shimadzu, Koichi Tanaka MS Research laboratory, Manchester, UK; Department of
MP 083	Discovery of G-Quadruplex DNA Binding Proteins Using MALDI-MS and LC/MS; Yuexi Wang; Linda McGown; Rensselaer Polytechnic Institute, Troy, NY Optimization of Chropopotide Conture for Biomerican	MD 002	Nuclear Medicine, Medical University, Vienna, Austria; ⁴ Department of Vascular Biology Thrombosis Research, Vienna, Austria Nanol C. MS/MS Analysis of Uniperv. Biomerkors for
MP 084	Optimization of Glycopeptide Capture for Biomarker Discovery in Human Plasma and Cerebrospinal Fluid; Frode Berven ^{1,2} ; Rushdy Ahmad ² ; Rune J Ulvik ¹ ; Steven A. Carr ² ; ¹ University of Bergen, Bergen, Norway; ² Broad Institute, Cambridge, MA	MP 093	NanoLC-MS/MS Analysis of Urinary Biomarkers for Chronic Graft-Versus-Host Disease; Michel Boutin ¹ ; Imran Ahmad ² ; Nathalie Lachapelle ² ; Claude Rondeau ² ; Jean Roy ² ; Pierre Thibault ¹ , ¹ IRIC, University of Montreal, Montréal, Canada; ² Blood and Marrow
MP 085	Proteomics and Protein Network Studies of Metastasis in Human Breast Cancer; Yashu Liu ¹ ; Jintang He ¹ ; Xiaolei Xie ¹ ; Steve Goodison ² ; David M.	MP 094	Transplant Program, HMR, Montréal, Canada Identifying Differentially Regulated Proteins as Markers for Colorectal Neoplasia.; Vikram Palamalai;

- Jonathan J Harrington; Douglas Mahoney; Ann L Oberg; H. Robert Bergen, Iii; David A Ahlquist; Mayo Clinic College of Medicine, Rochester, MN MP 095 **HIV-Infected Patients with Neurocognitive Impairments: Proteomic Fingerprints of** Serum/Plasma and CSF.; Jayme Wiederin¹; Fenghai Duan³; Wojciech Rozek²; <u>Pawel Ciborowski</u>¹; ¹University of Nebraska Medical Center, Omaha, NE; ²National Veterinary Research Instritue, Pulawy, Poland; ³Brown University, Providence, RI MP 096 Label-Free Proteomic Profiling of D-Serine-Induced
- Schlager; Pavel Shiyanov; Wright Patterson Air Force Research Laboratory, Dayton, OH MP 097 **Identification of Binding Partners in Eukaryotic**

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Translation Initiation Factors -RNA Binding Protein Complex.; David Shahbazian; Nahum Sonnenberg; Bernard F. Gibbs; McGill University, Montreal, Canada

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- MP 099 Discrimination among Geometrical Isomers of **Linolenic Acid Methyl Ester Using Low Energy Electron Ionization Mass Spectrometry and** Chemometrics; Diako Ebrahimi Mohammadi; Leila Hejazi; Michael Guilhaus; David B. Hibbert; The University of New South Wales, Sydney, Australia
- MP 100 **Determination of the Composition of Fatty Acid** Mixtures Using GC × FI-MS: A Comprehensive Two-Dimensional Separation Approach; Leila Hejazi; Diako Ebrahimi; Michael Guilhaus; David B. Hibbert; The University of New South Wales, Sydney, Australia
- MP 101 **Maximizing the Detection of Complex Hydrophobic** Lipids (e.g. triglycerides): Optimizing Ionization Efficiency and Chromatographic Standard Nanoscale Separations.; David A. Weil; Michael Woodman; Agilent Technologies, Schaumburg, IL
- MP 102 Singlet Oxygen Cycloadducts of Hydroperoxy Dienes Fragment to γ-Hydroxy Alkenals; A Reaction that is Promoted by Vitamin E; Xiaodong Gu; Wujuan Zhang; Jaewoo Choi; Wei Li; Xi Chen; James Laird; Robert G. Salomon; Case Western Reserve Univ., Cleveland, OH
- MP 103 Structure Characterization of Glycosphingolipids in **Human Milk**; <u>Ying Zhou</u>¹; David S. Newburg²; Catherine E. Costello¹; ¹Boston University School of Medicine, Boston, MA; ²Mass General Hospital Harvard Medical School, Boston, MA
- MP 104 **Chloro-Nitration of Biomembrane Lipids:** Arachidonic and Linoleic Acids; Srinivas Chakravartula; Archana Marathi; Michael Balazy; New York Medical College, Valhalla, NY
- MP 105 A New and Universal Product Ion Nomenclature for Low- and High-Energy CID of Sodiated Glycerophospholipid Precursor Ions; Ernst Pittenauer¹; Robert Mistrik²; Guenter Allmaier³; ¹Vienna University of Technology, Vienna, Austria; ²HighChem, Ltd., Bratislava, Slovakia; ³Vienna Univ of Technology, Vienna, Austria
- MP 106 **Analysis of Fatty Acid Methyl Esters Using the High** Throughput LDTD Source Coupled to the LTO **Orbitrap Mass Spectrometer**; Josee Champagne¹ André Vachereau³; <u>Sylvain Letarte</u>⁴; Denis Faubert¹; Pierre Picard²; ¹IRCM, Montreal, Canada; ²Phytronix Technologies, Inc., Quebec, QC; ³Dinotech Inc.,

- Roxboro, Canada; ⁴Phytronix Technologies, Blainville,
- MP 107 Automated Lipid A structure Hypotheses Generated by STALA: A Computational Tool to Interpret Lipid A Tandem Mass Spectra; Ying Sonia Ting¹; Scott A. Shaffer¹; Jace W. Jones¹; Wailap Ng²; Robert K. Ernst³; David R. Goodlett¹; ¹University of Washington, Seattle, WA; ²National Yang Ming University, Taipei, TAIWAN; ³University of Maryland, Baltimore, MD
- MP 108 Regiospecific Analysis of Triacylglycerols Using High Performance Liquid Chromatography/Electrospray **Ionization Tandem Mass Spectrometry of Sodiated** adduCts; Lisandra Cubero Herrera¹; Karen M. Glenn¹; Michael A. Potvin²; Jaroslav A. Kralovec²; Jeremy E. Melanson¹; ¹NRC Institute for Marine Biosciences, Halifax, Canada; ²Ocean Nutrition Canada, Halifax, Canada
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- MP 111 LC MS/IMS/MS of Chondroitin Sulfate Mixtures to Characterize Isomeric Forms; Roy Martin¹; Hui Wei¹; Joshua S. Sharp²; ¹Waters Corporation, Beverly, MA; ²University of Georgia, Athens, GA
- MP 112 Fast Sample Preparation for Sensitive Analysis of Helicobacter pylori Lipid A: Single Colony Analysis and Discovery of an Unusual Structure; Jianjun Li; Ping Zhou; Vandana Chandan; Xin Liu; Kenneth H.N. Chan; Eleonora Altman; National Research Council, Ottawa, Canada

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- MP 116 **Absolute Quantification of Oxidative Modifications** on apoA-I Protein by Stable Isotope Dilution LC-MRM/MS Assays; Kannan Rangiah; Eugene F. Ciccimaro; Ioannis Parastatidis; Harry Ischiropoulos; Muredach P Reilly; Sumit J Shah; Ian A Blair; University of Pennsylvania, Philadelphia, PA
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- Huan Wang; Won-A Joo; Tony Chang-Wong; David W. Speicher; *The Wistar Institute, Philadelphia, PA*
- MP 119 MRM for Oral Cancer Biomarker Validation in Saliva: Inherent Challenges, Solutions and Methods Development; Ebbing De Jong¹; Hongwei Xie²; Getiria I Onsongo¹; John V Carlis¹; Nelson L Rhodus¹; Frank G Ondrey¹; Tim Griffin¹; ¹University of Minnesota, Minneapolis, MN; ²Waters Corporation, Milford, MA
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 Vanbogelen¹; Michael R. Pisano¹; ¹NextGen Sciences, Ann Arbor, MI; ²ThermoFisher BRIMS, Cambridge, MA; ³Harvard Medical School, Boston, MA; ⁴Case Western University. Cleveland, OH
- MP 124 Multiplexed MRM Assay for the Detection of Prostate Cancer.; Anastasia K. Yocum^{1,2}; Rong Zhao^{1,2}; Arul M. Chinnaiyan^{1,2}, ¹University of Michigan, Ann Arbor, MI, ²Michigan Center for Translational Pathology, Ann Arbor, MI
- MP 125 The Discovery and Evaluation of Candidate Markers of Alzheimer's Disease Using Tandem Mass Tags and SRM Mass Spectrometry; Darragh O'Brien¹; Andreas Guentert²; Karsten Kuhn³; Peter Schulz-knappe³; Helen Byers¹; James Campbell¹; Simon Lovestone²; Malcolm Ward¹; Proteome Sciences PLC, London, UK; Institute of Psychiatry, London, UK; Proteome Sciences R&D, Frankfurt/ Main, Germany
- MP 126 Multiple Reaction Monitoring Cubed (MRM3): A
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 France; ³Applied Biosystems Germany, Darmstadt,
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- MP 127 Application of MRM and mTRAQ™ Labeling to the Verification Process of Candidate Biomarkers Discovered by Cleavable ICAT® Reagent; Un-Beom Kang¹; Younghee Ahn¹; Kyunggon Kim⁴; Jong Won Lee⁴; Yong-Hak Kim²; Byunghee Shin⁵; Sanghwa Kim⁵; Joon Kim³; Myeong-Hee Yu²; Youngsoo Kim⁴; Dong-Young Noh⁴; Cheolju Lee¹, ¹Life Sciences Division, KIST, Seoul, South Korea; ²Functional Proteomics Center, KIST, Seoul, South Korea; ³Korea University, Seoul, South Korea; ⁴College of Medicine, Seoul National University, Seoul, South Korea; ⁵Applied Biosystems, Seoul, South Korea

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 L.J. Sparvero¹; Shelly A. Kucherer²; Michael E. DeVera¹; Herbert J. Zeh¹; Michael T. Lotze¹; Andrew A. Amoscato¹; ¹University of Pittsburgh, Pittsburgh, PA;

 ²Carnegie Mellon University, Pittsburgh, PA
- MP 129 **Discovery, Verification and Multi-Technique Assay**of a New Serum Protein Biomarker of Ovarian
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- MP 130 A LC/MS/MRM Method for Insulin, Glucagon, Amylin Isoforms and GLP-1 Isoforms; Amy Lu; Albert B Seymour; Ru Wei; Pfizer RTC, Cambridge, MA

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- MP 133 Intact Protein Separation Using Alkaline Reversed Phase Chromatography for Proteomics; Hiroyuki Katayama; Yoshiya Oda; Eisai Co., Ltd., Tsukuba Ibaraki, Japan
- MP 134 Investigating the Apoptotic Proteome of Jurkat Cells
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- MP 135 Major Advance for 2D Fractionation of Intact
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 Catherman; Neil L. Kelleher; University of Illinois at
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- MP 136 Applying Reverse Electron Transfer Dissociation in the Mapping of Post-Translational Modifications in IDE and Tau Related to Alzheimer's Disease;

 Malwina A. Huzarska¹; Michael Easterling²; Desmond Kaplan²; Malcolm A. Leissring³; Nicolas Polfer¹;

 ¹University of Florida, Gainesville, FL; ²Bruker Daltonics, Inc., Billerica, MA; ³Mayo Clinic, Jacksonville, FL
- MP 137 Screening and Identification of Protein Mixture at One Time by Capillary LC/MALDI-TOF with Screening MALDI Plate; Junho Kim¹; Jongyeob Jeon³; Miyoung Ha^{2,3}; Yangsun Kim^{2,3}; ¹Department of Chemistry, Sangji University, Wonju, Korea; ²Hudson Surface Technology, Inc., Newark, NJ; ³Applied Surface Technologly, Inc., Suwon, Korea
- MP 138 A New Approach for Accurate Mass Top-Down Sequencing of Intact Proteins/Toxins Using High Resolution Ion-Trap TOF Mass Spectrometry; Christopher Nixon¹; Jesse Hines²; Timothy R. Croley¹; Icommonwealth of Virginia, DCLS, Richmond, VA; Shimadzu Scientific Instruments, Research Triangle Park, NC

- MP 139 **Top-Down PIITA Analysis and Bottom-Up PAcIFIC Analysis of Alpha Synuclein Isoforms**; Shu-Hua Chen;
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 David R. Goodlett; *University of Washington, Seattle,*WA
- MP 140 Unifying Fluorescence Microscopy and Mass Spectrometry for Studying Protein Complexes in Cells; Changhui Deng; Andrew Krutchinsky; UCSF, San Francisco. CA
- MP 141 In-Depth, Comprehensive Mapping of the Human Seminal Plasma Proteome by a Novel, Iterative LC-MS/MS/Database Search Workflow; Claire Dauly¹; Antoine D. Rolland²; Martin Hornshaw¹; Régis Lavigne³; Charles G. Pineau^{2,3}; ¹Thermo Fisher Scientific, Courtaboeuf Cedex, France; ²Inserm U625, Rennes, France; ³Proteomics Core Facility OUEST-genopole®, Rennes, France
- MP 142 MALDI TOF/TOF Data Acquisition Strategy that Minimizes MS/MS Acquisition Time While Maintaining High Quality Data and Increasing Depth of Coverage.; Kathleen Lewis¹; Aaron Booy²; Sean L. Seymour¹; Christie L Hunter¹; Applied Biosystems, Oakland, CA; MDS Analytical Technologies, Concord, ON
- MP 143 Comparison and Evaluation of Different Acquisition Parameters in LTQ-FT and LTQ-Orbitrap Mass Spectrometers to Improve Protein Identification Rates; Anastasia Kalli¹; Geoffrey Smith¹; John Lloyd²; Sonja Hess¹; ¹CalTech, Pasadena, CA; ²NIH/NIDDK, Germantown, MD
- MP 144 A Data-Dependent Method to Increase Protein
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 Annan; GlaxoSmithKline, King of Prussia, PA
- MP 145 Comparison of Gas Phase Fraction, Precursor Ion Exclusion and On-Line SCX Separation on Limited Amount Proteome Samples Analysis; Wei Chen; University of British Columbia, Vancouver, Canada
- MP 146 Generating Products of All Ions Using a High Speed and High Sensitivity Experimental Trap-TOF.;

 Stephen A Tate¹; Nic Bloomfield²; Igor Chernushevich³; Alexandre Loboda³; ¹MDS Sciex, Concord, Canada; ²MDS Analytical Tech-Sciex, Concord, ON; ³MDS Analytical Technologies, Concord, ON
- MP 147 Improved Sampling of complex Mixtures Using Data-Independent Acquisition on an Ion Trap Mass Spectrometer Equipped with an Ion Funnel; Jesse D. Canterbury; Scott A. Shaffer; Gennifer E. Merrihew; David R. Goodlett; Michael J. Maccoss; University of Washington, Seattle, WA
- MP 148 Using High Resolution Ion Maps as an Alternative to Low Resolution MRM for Validating Proteins in Complex Matrices; Scott Geromanos; Marc V. Gorenstein; Jim Langridge; Waters Corporation, Milford. MA
- MP 149 Data-Independent (PAcIFIC) Direct Infusion
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- MP 150 Workflow for Maximizing Proteome Coverage Using CID and ETD; Martin Zeller; Bernard Delanghe;

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- MP 151 Increased Sequence Coverage in Complex Protein
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 TX; ²Bruker Daltonics, Bremen, Germany; ³Bruker
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- MP 152 Practical Advantage of Negative Ion Mode MALDI:
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 Tohoku University, Sendai, Japan
- MP 153 In-Source Atmospheric Pressure Electron Capture Dissociation (AP-ECD): Applicability for the Study of Post-Translational Modifications on Peptides;

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- MP 154 Intermediate Pressure MALDI-FTMS for
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 **IUniversity of Rochester Medical Center, Rochester, NY;
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 ¹Shimadzu International Trading(Shanghai)Co., Limit, Beijing, China; ²China Agricultural University, Beijing, China
- MP 156 Ultra High Mass Resolution and Mass Accuracy Measurement and Multistage MS on Structural Elucidation of Trace Level Pharmaceutical Impurities; Wendy Zhong¹; Jiong Yang¹; Michael Easterling²; ^ISchering-Plough, Summit, NJ; ²Bruker Daltonics, Inc., Billerica, MA
- MP 157 Using Iso-LCMS for Impurity Identification Directly from a Non-Volatile Mobile Phase Buffer by LCMS Linear Ion Trap Technology; Jeffrey M. Selenka; Thomas Leitzinger; Cynthia Sanderson; PPD, Middleton, WI
- MP 158 **Determination of Repaglinide in Human Plasma**Using Positive Ion ESI-LC/MS/MS; Hollie Barton;
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 Hidy; Rand Jenkins; PPD, Richmond, VA
- MP 159 FAIMS for Drug Discovery and Development Using an Ion Trap and a Triple Quadrupole MS.; Keeley Murphy; Kevin Cook; Julie Horner; James Kapron; Nicholas Duczak, Jr; Mark Harrison; Thermo Fisher Scientific, San Jose, CA
- MP 160 Simultaneous Determination of Emtricitabine and Tenofovir in Human Plasma Using Positive Ion ESI-LC/MS/MS; Moucun Yuan; Laura Nakovich; William R. Mylott; Bruce Hidy; Rand Jenkins; PPD, Richmond, VA
- MP 161 Characterization of Degradation Products of a
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 Dennis Hill¹; David Grant¹; **Iuniversity of Connecticut,
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- Thomas Brenna; Cornell University, Ithaca, NY
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- MP 165 Determination of Triamcinolone Acetonide in Human Plasma Using Liquid-Liquid Extraction and High-Performance Liquid Chromatography Coupled to Tandem Mass Spectrometry (LC-MS/MS).; Rafael E. Barrientos-Astigarraga; Paulo A. R. Galvinas; Jane K. Finzi; Maria Fernanda de O. Carrazedo; Yara Popst Armando; Leandro S. C. Barbosa; Olívia C. M. Amorim; Washington M. Silva; MAGABI Pesquisas Clinicas Farmaceuticas Ltda., São Paulo, Brazil
- MP 166 High Performance Liquid Chromatography
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 Haiyan Gao¹; Jing Dong³; Feng Feng²; Leren Wan³;
 Yuki Hashi³; Hailin Wang²; ¹Central South University,
 Changsha, China; ²Research Center of Ecoenviromental sciences, Beijing, China; ³Shimadzu
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 China
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			Taiwan; ² Kaohsiung Medical University, Kaohsiung,
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	Biosystems Inc., Sao Paulo, Brazil; ² MDS Analytical		Sumit Shah; Ian A. Blair; Center for Cancer
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MP 285 **Top-Down ECD Mass Spectrometry of Calmodulin Deamidation**; Chunxiang Yao¹; Nadezda P. Sargaeva¹; Weidong Cui¹; Xiaojuan Li¹; Tzu-yung Lin¹; Konstantin Aizikov¹; Cheng Lin¹; Peter B. O'connor²; Boston University Sch Med, Boston, MA; University of Warwick, Coventry, UK

MP 286 An Integrated Bottom-Up and Top-Down Characterization of Metalloproteins and Protein Molecular Forms in the Extracellular Fraction of Extremophilic Microbial Communities; Brian K.

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MP 289 A Mixed-Integer Linear Optimization Framework for the Identification and Quantification of Highly Modified Proteins via Electron Transfer Dissociation Tandem MS; Peter A. DiMaggio; Nicolas L. Young; Richard C. Baliban; Benjamin A. Garcia; Christodoulos A. Floudas; Princeton University, Princeton, NJ

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MP 291 Protein LC-MS with On-Line Fraction Collection,
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MP 292 Application of an Intact Protein Separation Space for PTM Characterization; Mark E. McComb; David H. Perlman; Wantao Ying; Giuseppe Infusini; Vivek N. Bhatia; Weiwei Tong; Catherine E. Costello; Boston University School of Medicine, Boston, MA

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MP 294 Microwave-Assisted Acid Hydrolysis Combined with LC-ESI QqTOF MS for Mapping Complete Protein Sequences and Characterizing PTMs; Nan Wang; Liang Li; University of Alberta, Edmonton, Alberta, Canada

MP 295 **PTM Finder Based on PEAKS De Novo Sequencing Result**; Lei Xin¹; Baozhen Shan²; Gilles Lajoie³; Bin Ma⁴; ¹CS Dept. of The University of Western Ontario, London, Canada; ²Bioinformatics Solutions Inc., Waterloo, ON; ³University of Western Ontario, London, ON; ⁴University of Waterloo, Waterloo, ON

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MP 297 Characterizing Protein Post-Translational
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MP 299 An Unbiased Tale of *in vitro* Modifications: In-Depth Analysis of Artifacts Caused by Proteomics Sample Preparation; Michael L. Nielsen; Juergen Cox; Jesper V. Olsen; Matthias Mann; *Max-Planck-Institute for Biochemistry, Martinsried (near Munich), Germany*

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 ¹University of British Columbia, Vancouver, Canada;

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 ¹National Research Council, Segrate (MI), Italy; ²ISB srl, Milan, Italy; ³National Cancer Institute Foundation, Milan, Italy
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	L Wentzel; Tandem Labs, West Trenton, NJ		Wareham, MA
MD 250		MP 372	Extraction of Melamine from Various Matrices Using
MP 359	Dried Blood Spots Assays for Determination of	5,2	Resin-Based Mixed-Mode Cation Exchange SPE and
	Various Drugs in Whole Blood by LC-MS/MS;		Analysis with LC-MS/MS.; Lee Williams ¹ ; Elena
	Xiaorong Liang ¹ ; Glenn Hanson ¹ ; Tom Addison ¹ ; Julie		
	Tollefson ¹ ; Kevin Jones ¹ ; David M. Bakes ² ; Lee		Gairloch ² ; Rhys Jones ¹ ; Helen Lodder ¹ ; Steve Jordan ¹ ;
	Goodwin ² ; Phillip Turpin ² ; ¹ Covance, Madison, WI;		Richard Calverley ¹ ; Claire Desbrow ¹ ; Steve Plant ¹ ; Gary
	² Covance Laboratories Ltd, Harrogate, UK		Dowthwaite ¹ ; Joanna Caulfield ¹ ; ¹ Biotage GB Limited,
MP 360	Evaluate and Solve an Unusual differential Recovery		Cardiff, UK; ² Biotage, Charlottesville, VA
	Problem in Bioanalysis of a Boron-Containing	MP 373	A New Online SPE/LC/MS/MS Method for Screening
	Compound in Mouse Blood; Ji Zhang; Michael		Perfluorinated Compounds (PFCs) in Waste Water;
	Johnson; Cindy Xia; Mark Qian; Millennium: The		<u>Fredrick D. Foster</u> ¹ ; Meike Baden ² ; Norbert Helle ² ;
	Takeda Oncology Company, Cambridge, MA		Juergen Wendt ³ ; ¹ Gerstel GmbH & Co KG, Mülheim an
MP 361	Multi-Class Antibiotic Screening of Honey Using		der Ruhr, Germany; ² TeLA GmBH, Bremerhaven,
WIF 301			Germany; ³ Agilent Technologies, Waldbronn, Germany
	Dual On-line Extraction Columns in Tandem;	MP 374	Human Plasma Renin Activity Assay with On-Line
	Catherine Lafontaine; Yang Shi; Francois A.	1411 371	Solid Phase Extraction and LC/MS/MS Detection;
	Espourteille; Thermo Fisher Scientific, Franklin, MA		Kheng B. Lim ¹ ; Daniel B. Kassel ¹ ; ¹ Takeda San Diego,
MP 362	C18-Functionalized Magnetic Nanoparticles as		
	Extraction Sorbent Combined with LC-MS for	N 6D 2775	Inc., San Diego, CA
	A 1	MP 375	Improved Extraction for the Quantitation of Plasma
	Analysis of Benzophenones in Urine Sample; Tzung-		
			Total F2-Isoprostanes; Alan W. Taylor; Maret G.
	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National		
MP 363	Jie Yang; <u>Pei-Cheng Wang</u> ; Maw-rong Lee; <i>National Chung-Hsing University, Taichung, Taiwan</i>		Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR
MP 363	Jie Yang; <u>Pei-Cheng Wang</u> ; Maw-rong Lee; <u>National Chung-Hsing University</u> , <u>Taichung</u> , <u>Taiwan</u> Determination of Nimetazepam and Metabolites in	MP 376	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380
MP 363	Jie Yang; <u>Pei-Cheng Wang</u> ; Maw-rong Lee; <u>National Chung-Hsing University</u> , <u>Taichung</u> , <u>Taiwan</u> Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS ; <u>Chun-Hung Wang</u> ; Ren-	MP 376	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human
MP 363	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing	MP 376	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem
	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan	MP 376	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral
MP 363	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in	MP 376	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu
	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in Liquid Chromatography-Electrospray Ionization		Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu Jiang; Covance Laboratories Inc., Madison, WI
	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometric Quantification of	MP 376	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu Jiang; Covance Laboratories Inc., Madison, WI A Chiral LC-MS/MS Method for the Separation and
	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometric Quantification of Hydroxysteroids; Kouwa Yamashita; Keiko Yamazaki;		Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu Jiang; Covance Laboratories Inc., Madison, WI A Chiral LC-MS/MS Method for the Separation and Quantitation of Lorcaserin and Its S-Enantiomer;
	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometric Quantification of Hydroxysteroids; Kouwa Yamashita; Keiko Yamazaki; Madoka Takahashi; Mitsuteru Numazawa; Tohoku		Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu Jiang; Covance Laboratories Inc., Madison, WI A Chiral LC-MS/MS Method for the Separation and Quantitation of Lorcaserin and Its S-Enantiomer; Michael Ma; WeiChao Chen; Yong Q. Tang; Arena
MP 364	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometric Quantification of Hydroxysteroids; Kouwa Yamashita; Keiko Yamazaki; Madoka Takahashi; Mitsuteru Numazawa; Tohoku Pharmaceutical University, Sendai, Japan	MP 377	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu Jiang; Covance Laboratories Inc., Madison, WI A Chiral LC-MS/MS Method for the Separation and Quantitation of Lorcaserin and Its S-Enantiomer; Michael Ma; WeiChao Chen; Yong Q. Tang; Arena Pharmaceuticals, San Diego, CA
	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometric Quantification of Hydroxysteroids; Kouwa Yamashita; Keiko Yamazaki; Madoka Takahashi; Mitsuteru Numazawa; Tohoku Pharmaceutical University, Sendai, Japan Sensitivity Enhancement in UPLC/MS/MS for		Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu Jiang; Covance Laboratories Inc., Madison, WI A Chiral LC-MS/MS Method for the Separation and Quantitation of Lorcaserin and Its S-Enantiomer; Michael Ma; WeiChao Chen; Yong Q. Tang; Arena Pharmaceuticals, San Diego, CA Use of Normal Phase Chromatography to Enhance
MP 364	Jie Yang; Pei-Cheng Wang; Maw-rong Lee; National Chung-Hsing University, Taichung, Taiwan Determination of Nimetazepam and Metabolites in Urine by LC-APCI/MS/MS; Chun-Hung Wang; Ren- Jye Lee; Maw-Rong Lee; National Chung-Hsing University, Taichung, Taiwan Use of Fusarate as a Highly-Sensitive Derivative in Liquid Chromatography-Electrospray Ionization Tandem Mass Spectrometric Quantification of Hydroxysteroids; Kouwa Yamashita; Keiko Yamazaki; Madoka Takahashi; Mitsuteru Numazawa; Tohoku Pharmaceutical University, Sendai, Japan	MP 377	Total F2-Isoprostanes; Alan W. Taylor; Maret G. Traber; Oregon State University, Corvallis, OR CHIRAL ANALYSIS BY MS, 376 - 380 Determination of Metoprolol Enantiomers in Human Plasma by Liquid Chromatography with Tandem Mass Spectrometry Using Cellobiohydrolase Chiral Stationary Phase; Xi Chen; Hongliang Jiang; Xiang-yu Jiang; Covance Laboratories Inc., Madison, WI A Chiral LC-MS/MS Method for the Separation and Quantitation of Lorcaserin and Its S-Enantiomer; Michael Ma; WeiChao Chen; Yong Q. Tang; Arena Pharmaceuticals, San Diego, CA

- 57th ASMS Conference on Mass Spectrometry Nicolas Jean; Chantal Gravel; Sylvain Lachance; Ann Levesque; Robert Masse; Anapharm, Québec, Canada MP 379 Chiral LC-MS/MS Analysis with Polysaccharide **Based Stationary Phases Using Novel Mobile Phases** in RP Elution Mode for Stereoisomeric Pharmaceutical Compounds; Liming Peng; Tivadar Farkas; Swapna Jayapalan; Phenomenex, Inc., Torrance, MP 380 **Charge-State-Dependent Enantioselective** Discrimination of Leucine Enantiomers by Antimony(III)-D/L-Tartrate Elucidated by ESI-MS, Computational Modeling and 1H-NMR.; Aruna B. <u>Wijeratne</u>¹; Jose Gracia²; Daniel W. Armstrong¹; Kevin A. Schug¹; ¹University of Texas at Arlington, Arlington, TX; ²Schuit Inst. of Catalysis, Eindhoven University, Eindhoven, Netherlands **IMMUNOLOGY, 381 - 396** MP 381 **Detection of Signal Peptides Presented by HLA-**A*0201 in TAP Competent Cells using Nanospray MS3 on a Linear Ion Trap; Bruce B. Reinhold¹; Song Ye²; Ellis Reinherz¹; ¹Dana Farber Cancer Institute, Boston, MA; ²Applied Biosystems, Framingham, MA MP 382 **Evaluating the Antigenicity of Cancer Therapeutic** Immunotoxins Using MS-Based Epitope Mapping; James G. Smedley, III¹; Johanna Hansen²; Masanori Onda²; Ira Pastan²; Kenneth B. Tomer¹; ¹NIEHS, Research Triangle Park, NC; ²NCI, Bethesda, MD The Effect of Interferon-gamma on the Proteome and MP 383 the MHC-Peptidome of Human Carcinoma Cells; Elena Milner¹; Eilon Barnea¹; Ilan Beer²; Arie Admon¹; ¹Technion - Israel Institute of Tech, Haifa, Israel; ²IBM Research Laboratory, Haifa, Israel MP 384 **Identification of Novel MHC Class I Presented Epitopes in Lung Cancer by Mass Spectrometry**; Punit Shah; Vivekananda Shetty; Thamby Gomathinayagam; Zacharie Nickens; Ramilla Philip; Immunotope, Inc., Doylestown, PA MP 385 MS Analysis of the MHC II Peptide Repertoire of
- Cell-Based Cancer Vaccines in the Presence or
 Absence of Invariant Chain.; Olesya Chornoguz;
 Alexei Gapeev; Suzanne Ostrand-Rosenberg; UMBC,
 Baltimore, MD

 MP 386 Utilizing Secreted MHC Molecules (sHLA) to
 Investigate the Phospho-Immuno-Peptidome of
- MP 386 Utilizing Secreted MHC Molecules (sHLA) to Investigate the Phospho-Immuno-Peptidome of Breast Cancer; Andrew Norris¹; A. Michelle English¹; Jie Qian¹; Oriana E. Hawkins²; Victor H. Engelhard¹; Jeffrey Shabanowitz¹; William Hildebrand²; Donald F. Hunt¹; ¹University of Virginia, Charlottesville, VA; ²University of Oklahoma, Oklahoma City, OK
- MP 387 Quantitative Proteomic Analysis Using SILAC
 Reveals Compartment-Specific Interactions of T-Cell
 Specific Ligand (TULA/STS-2); Therese
 Collingwood^{1,2}; Alexander Tsygankov¹; Roland S.
 Annan^{1,2}, ¹Temple University School of Medicine, Phila,
 PA; ²GlaxoSmithKline, King of Prussia, PA
- MP 388 Profiling of Real-Time and Dynamic Changes of MyD88 Interactions for Mediating Innate Immune Response by Using iTRAQ and SILAC; Sun Yong Jeong; Yanbao Yu; Xian Chen; University of North Carolina, Chapel Hill, NC
- MP 389 Organelle Membrane Proteomics Reveals New Insights on Phagosome Maturation Mediated by Mycobacterial Lipoglycans; Wenqing Shui²; Chris Petzold¹; Alyssa Redding¹; Austin Pitcher²; Leslie Sheu³; Tsung-yen Hsieh³; Jay D. Keasling^{1,4}; Carolyn R. Bertozzi^{2,3}; ¹Lawrence Berkeley National Lab, Berkeley,

- CA; ²Department of Chemistry, UC Berkeley, Berkeley, CA; ³Department of Molecular & Cell Biology, UC Berkey, Berkeley, CA; ⁴Department of Chemical Engineering, UC Berkeley, Berkeley, CA
- MP 390 Quantitative Phosphoproteomics: Deciphering the Essential Role of Gab2 in Mast Cell Signaling.; <u>Lulu Cao</u>¹; Kebing Yu¹; Vinh Nguyen²; Arthur Salomon²; **Ibrown University Chemistry Department, Providence, RI; **2Brown University MCB Department, Providence, RI
- MP 391 The Use of Mass Spectrometry in Immunoassay
 Development for Nonclinical and Clinical Studies;
 Ola M. Saad; Jakub Baudys; Keyang Xu; Luna Liu;
 Cecilia Leddy; Surinder Kaur; Genentech, Inc., South
 San Francisco, CA
- MP 392 Multiplex Analysis of Food Allergens Using
 Immunoprecipitation and Mass Spectrometry; Kevin
 J. Shefcheck¹; Jinxi Li²; Catherine Fenselau²; John H.
 Callahan¹; Steve Musser¹; ¹FDA/CFSAN, College Park,
 MD; ²University of Maryland, College Park, MD
- MP 393 High Throughput Bioinformatic and Proteomic Platform to Identify Viral Virulence Genes and Their Cellular Targets; Refugio Martinez; VLST Corporartion, Seattle, WA
- MP 394 Antibody-Antigen Binding Affinity Measurement Using HD Exchange and Dilution Strategy; Tingting Tu¹; Don L. Rempel¹; Alina Petre²; Michael Przybylski²; Michael L. Gross¹; ¹Washington University in St. Louis, Saint Louis, MO; ²University of Konstanz, Konstanz, Germany
- MP 395 A Temporal Analysis of the Bovine Innate Immune Response: The Identification and Characterization of Antimicrobial Peptides by Mass Spectrometry;

 Jeffrey A. DeGrasse¹; Jamie L. Boehmer²; Kevin J. Shefcheck¹; Jeffrey L. Ward²; John H. Callahan¹;

 ¹FDA/CFSAN, College Park, MD; ²FDA/CVM, Laurel,
- MP 396 Relative Quantification of Differentially Expressed Proteins in Bovine Milk during Coliform Mastitis Using Spectral Count Data; Jamie L. Boehmer¹; Jeffrey L. Ward¹; Douglas D. Bannerman²; Kevin J. Shefcheck³; Melinda A. Mcfarland³; John H. Callahan³; ¹FDA Center for Veterinary Medicine, Laurel, MD; ²Department of Veterans Affairs, Washington, DC; ³FDA/CFSAN, College Park, MD

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- MP 397 Evaluation of QTOF Technology for the Quantitation of Drugs in Plasma; Julie Marr¹; Walter Korfmacher²; Fangbiao Li²; Yunsheng Hsieh²; Bob Walker¹; Jim Lau¹; ¹Agilent Technologies, Mississauga, Canada; ²Schering-Plough, Kenilworth, NJ
- MP 398 Quantitation of Analytes with a QTOF Versus a QQQ Instrument. How Big is the Penalty for Qualitative Information?; Sian L Avery; Angela Hayes; Frederique Urban; Florence I. Raynaud; The Institute of Cancer Research, Sutton, UK
- MP 399 The Potential for High Resolution Mass Analyzers for Quantification in Pharmaceutical Bioanalysis;

 Panos Hatsis; Wilmin P. Bartolini; Robert Busby;

 Ironwood Pharmaceuticals, Cambridge, MA
- MP 400 Screening and Semi-Quantitative Analysis for Pharmaceutical Drug Metabolites in Urine Samples;

 Yoshifumi Kogure; Masahiro Maeda; Yoshiyuki Ishii;

 Agilent Technologies, Hachioji, Japan
- MP 401 Development of a Quantitative Chiral HPLC/MS
 Method to Investigate Secondary Alcohol
 Epimerization Process Using LC/ Ion Trap FT-MS;

	MONDIN	TOSTERS	
	Hong Cai; Chiuwa Emily Luk; Xiang-Yang Ye; Jun Dai;		Seo Hyun Yoon; Kyung-Sang Yu; In-Jin Jang; Seoul
	Bogdan Sleczka; Angela K. Goodenough; Jonathan L.		National University, Seoul, South Korea
	Josephs; Bristol-Myers Squibb, Pennington, NJ	MP 413	Validation of a Method for the Determination of
MP 402	Super-Critical Fluid Chromatography (SFC) with		Lapatinib in Human Plasma by LC-MS/MS; Robb
	Tandem Mass Spectrometry (MS/MS) to Evaluate		Harman; Hongkun Liang; Yongdong Zhu; Yuan-shek
	the Disposition of Individual Stereo-Isomers of		Chen; Kumar Ramu; QPS, LLC, Newark, DE
	Drugs; Qing Ping Han; Xu Zhang; David P. Budac;	MP 414	Quantitative LC-MS/MS Determination of
	Mark J. Hayward; Silke Miller; Lundbeck Research		Melphalan in Human Plasma; Jared Callan; Hongli
	USA, Paramus, NJ		Wang; Yuwen Zhao; Jamie Zhao; Yuan-Shek Chen;
MP 403	Determination of Resveratrol and its Metabolites in		Kumar Ramu; QPS, LLC, Newark, DE
	Rat Fetus and Pup Tissues by UPLC-MS/MS;	MP 415	Determination of 6-Benzylthioinosine in Human and
	Melanie A. Rehder Silinski ¹ ; Franz K. Thomas ¹ ; James		Mouse Plasma by LC-ESI-MS/MS; Lan Li; Cleveland
	C. Blake ¹ ; Reshan E. Fernando ¹ ; Richard Daw ¹ ; Timothy		State University, Cleveland, OH
	R. Fennell ¹ ; Brian F. Thomas ¹ ; Bradley J. Collins ² ; ¹ RTI	MP 416	Simulataneous Quantiation of Methotrexate and its
	International, Research Triangle Park, NC;		Metabolite 7-Hydroxymethotrexate in Human
	² NIEHS/National Toxicology Program, Research		Plasma by LC/MS/MS Combined with Solid Phase
	Triangle Park, NC		Extraction; Xiaoping Ao; Jamie Zhao; Lina Tang;
MP 404	UPLC-MS/MS Analysis of Nitroglycerin and		Hsun-Wen Chou; Yuan-shek Chen; Kumar Ramu; QPS,
	Metabolites in Human Plasma; Dale A. Raines; G.		LLC, Newark, DE
	Paul Brown; Jonathan O. Rathe; John G. Rollag; Chris J.	MP 417	Quantitative Determination Of Temozolomide In
	Kafonek; Alan M. Dzerk; Curtis E. Sheldon; Chad J.		Human Plasma By LC/MS/MS; Hongkun Liang;
	Briscoe; MDS Pharma Services, Lincoln, NE		Bashir A. Mansoori; Crystal Nguyen; Robert Harman;
MP 405	Determination of Clozapine and its Two Metabolites		Yongdong Zhu; Kumar Ramu; QPS, LLC, Newark, DE
	in Rat Plasma and Brain Tissue Using Ultra-	MP 418	Determination of Moxifloxacin used as Positive
	Performance Liquid Chromatography/Tandem Mass		Controls for QT Prolongation in Human Plasma by
	Spectrometry; Feng Liang ¹ ; Alvin V. Terry ² ; Michael		LC-MS/MS; Lina Tang; Yuwen Zhao; Kristen
	G. Bartlett ¹ ; ¹ University of Georgia, Athens, GA;		Singleton; <u>Jerry Cao</u> ; Jamie Zhao; Yongdong Zhu;
100	² Medical College of Georgia, Augusta, GA		Yuan-shek Chen; Kumar Ramu; QPS, LLC, Newark, DE
MP 406	Metabolic Stability Study Using Cassette Analysis	MP 419	Quantification of Doxorubicinol with the Presence of
	and Polarity Switching in an Ultra High Performance		Excessive Doxorubicin in Human Plasma by Column
	Liquid Chromatography (UHPLC)-Triple		Switching and LC-MS/MS Techniques; Moo-young
	Quadrupole System ; Anabel Fandino ¹ ; Edgar Naegele ¹ ; Stephan Buckenmaier ² ; Bernd Glatz ¹ ; ¹ Agilent		Kim; Yansheng Liu; Ying Li; Sarah Swenson; Gene
	Technologies, Santa Clara, CA; ² Agilent, Waldbronn,	MP 420	Ray; Dari Dadgar; AAI Pharma, Shawnee, KS
	Germany	WIF 420	Determination of Capsaicin and in Human Plasma by LC-MS/MS Following 96-Well Liquid-Liquid
MP 407	Quantitative Open Access LC-MS/MS Using		Extraction; Changyu Quang; Xiaodong Zhu; Tom
WII 407	QuickQuan and QuickCalc Software.; John G.		Addison; John Banach; Xiang-yu Jiang; Kevin Jones;
	Swales; Gary Wilkinson; Astrazeneca, Macclesfield, UK		Covance Bioanalytical Servic, Madison, WI
MP 408	Rapid Method Development and Evaluation for	MP 421	Quantitative HPLC-ESI-MS/MS Analysis of bis-N7-
1111 100	Bioanalysis in Drug Discovery; Hongying Gao; Max	21	Guanine Cross-Links in White Blood Cells of Cancer
	Tella; Brian Rago; Steven Hansel; Christopher		Patients Receiving Cyclophosphamide Therapy;
	Holliman; Pfizer Inc, Groton, CT		Bhaskar Malayappan; Natalia Tretyakova; University of
MP 409	LDTD-MS/MS Analysis of Eicosanoids and Other		Minnesota, Minneapolis, MN
	Mediators of Inflammation; Pierre Picard ³ ; Serge	MP 422	Optimization of On-Line Coupling of Weak Anion-
	Picard ² ; Nicolas Flamand ⁴ ; Katherine Boulay ² ; <u>E. Real</u>		Exchange and Ion-Pair HPLC Systems for Robust
	<u>Paquin</u> ¹ ; Pierre Borgeat ² ; ¹ Universite Laval, Quebec,		and Sensitive MS/MS Detection of Nucleotide
	Canada; ² Centre de Recherche en Rhumatologie et		Triphosphates; Zsuzsanna Kuklenyik; Angela Holder;
	Immunologie, Québec, Canada; ³ Phytronix		Ae S. Youngpairoj; Mian-er Cong; Qi Zheng; Gerardo
	Technologies, Inc., Quebec, QC; ⁴ Centre de Recherche		Garcia-Lerma; Walid Heneine; James L. Pirkle; John R.
	de l'hôpital Laval, Québec, Canada		Barr; Centers for Disease Control and Prevention,
MP 410	Determination of Acetylsalicylic Acid and Salicylic		Atlanta, GA
	Acid in Human Plasma BY LC/MS/MS; Hongkun	MP 423	Determination of Ibandronate (a Complex
	<u>Liang</u> ; Mojdeh Vahid; Yongdong Zhu; Jamie Zhao;		Biophosphonate) in Human Plasma by LC/MS/MS;
	Kristen Singleton; Preeta Bissessar; Yuan-Shek Chen;		Kristen Singleton; Jasper X. Chu; Jared Callan; Preeta
	Kumar Ramu; Quest Pharmaceutical Service, Newark,		Bissessar; Yuan-shek Chen; Kumar Ramu; QPS, LLC,
1 (D. 444	DE	N (D) (D)	Newark, DE
MP 411	Quantitation of Free Quercetin in Human Whole	MP 424	On-Line Sample Enrichment, Cleanup, and
	Blood by HPLC-MS/MS; Yuwen Zhao; Lina Tang;		Phospholipids Removal Using Protein Precipitation
	Jamie Zhao; Yuan-shek Chen; Kumar Ramu; <i>QPS, LLC,</i>		for Microdosing Bioanalysis; Fumin Li; John Zulkoski;
MD 412	Newark, DE		Wes Brown; Xiangyu Jiang; Tom Addison; Jacob
MP 412	Simultaneous Quantification of Paclitaxel and	MD 425	Maguigad; Kevin Jones; Covance Inc., Waunakee, WI
	Metabolites in Human Plasma by Liquid	MP 425	Effect of Storage and Freeze / Thaw Cycles on
	Chromatography-Tandem Mass Spectrometry (LC-		Plasma Enzyme Activity, Phospholipids and pH in
	MC/MC). Saul Oh: Have Sult Vim. In hore Shine.		FDTA Human Plasma: Stavan T W.1. Thomas
	MS/MS); Seul Oh; Hwa Suk Kim; Jun-hwa Shim;		EDTA Human Plasma; Steven T. Wu ¹ ; Zheng
	MS/MS); <u>Seul Oh</u> ; Hwa Suk Kim; Jun-hwa Shim; Hyang-Hee Yang; Won-Seok Nam; Seon-Jeong Kim;		EDTA Human Plasma; Steven T. Wu ¹ ; Zheng Ouyang ¹ ; Mohammed Jemal ¹ ; ¹ Bristol-Myers Squibb, Princeton, NJ

MP 426	Comparison of Three MS/MS Techniques for	
	Monitoring Plasma Phospholipids and Effect of	
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Yuan-qing Xia; Mohammed Jemal; Bristol-Myers		
	Squibb Company, Princeton, NJ	

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- MP 427 An Alternative Screening Strategy for Drug Discover Using Accurate Mass; Mark Szewc; Josef Ruzicka; Mark Sanders; Thermo Fisher Scientific, Somerset, NJ
- MP 428 Application of an LC-Orbitrap Approach to Complete Metabolite Identification in 2 Injections;

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- MP 429 Comparison of Three High-Throughput Methods for the Simultaneous Measurement of Metabolic Stability and Identification of Metabolites; Alek N. Dooley; Alexandre Wang; Hua-fen Liu; Elliott Jones; Loren Olson; Applied Biosystems, Foster City, CA
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- MP 432 Characterization of CVT-3619 Metabolites in Rat
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- MP 434 The Versatility of Parallel HPLC, Data Acquisition and Processing Workflows for Enhanced LC/MS/MS Throughput in Early Drug Discovery; Veronica Zelesky; Richard Schneider; John Janiszewski; Pfizer Inc., Groton, CT
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- MP 438 Evaluation of Accurate Mass TOF-MS for use in High Throughput CYP450 Inhibition Screening;

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- MP 441 Real Time Neutral Loss IDA Trigger on High
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 Nic Bloomfield²; Eva Duchoslav¹; ¹MDS Analytical
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- MP 442 High Throughput Identification of Irinotecan
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 1 University of Alabama at Birmingham, Birmingham, AL; 2 University of California, Los Angeles, Los Angeles, CA
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	² Thermo Scientific, San Jose, CA	MP 469	Understanding Hydrophobicity and Limits of
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	³ Michrom Bioresources, Inc., Auburn, CA	MP 474	Highly Sensitive Peptidomics Profiling of Native
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- MP 479 The Caenorhabditis elegans Bacterial Resistant bus-2
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- MP 487 **Determination of Linkages of Oligosaccharides Using**Closed-Ring 8-aminopyrene-1,3,6-trisulfonate
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- MP 488 Alterations in the Glycomics of Major and Minor Proteins Fractionated from the Serum of Hepatocellular Carcinoma Patients; Pilsoo Kang¹; Milan Madera¹; William R Alley¹; Radoslav Goldman²; Yehia Mechref¹; Milos V Novotny¹; Indiana University, Bloomington, IN; Georgetown University, Washington, DC
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- MP 491 MALDI and ESI of Oligosaccharides and Their Glycopeptides Conjugates; Yu-Ling Chang¹; Sylvain Liao²; Wen-Bin Yang²; Yuan-Chuan Lee³; Chung-Hsuan Chen^{1,2}; ¹Department of Chemistry, National Taiwan University, Taipei, Taiwan; ²Genomics Research Center, Academia Sinica., Taipei, Taiwan; ³Department of Biology, Johns Hopkins University, Baltimore, MD
- MP 492 A Mass Spectrometry Based Glycomic Approach for Identification of Carbohydrate Dependant Virulence Factors Using Caenorhabditis Elegans as a Surrogate Host; Md Mizanur Rahman¹; Jonathan Hodgkin²; John F Cipollo¹; ¹Food and Drug Administration/CBER, Bethesda, MMD; ²University of Oxford, Oxford, UK
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	Squibb, Wallingford, CT Optimized Condition to Capture Peptides (Bradykinin and Buccalin) for Efficient Fractionation of a Peptide/Protein Mixture; Ven Ney Wong; Gary R. Kinsel; Daniel Dyer; Southern Illinois University Carbondale, Carbondale, IL Online Analysis of Metal-Binding Peptides Using an Ion-Selective Membrane Probe Coupled to ESI-MS TOF; Juan Astorga-Wells ^{1,2} ; Thomas White ³ ; Craig M.		Medicine, Bronx, NY REACTIVE METABOLITES, 517 - 535 High Throughput Screening GSH Adducts Using Hybrid Linear Ion Trap Systems Coupling with Fast Chromatography at Clinically Relevant Dose Concentration; Elliott Jones ¹ ; Claire Bramwell- German ¹ ; Hesham Ghobarah ² ; Hua-fen Liu ¹ ; ¹ Applied Biosystems, Foster City, CA; ² Applied Biosystems / MDS Sciex, Concord, ON
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MP 505 MP 506	Squibb, Wallingford, CT Optimized Condition to Capture Peptides (Bradykinin and Buccalin) for Efficient Fractionation of a Peptide/Protein Mixture; Ven Ney Wong; Gary R. Kinsel; Daniel Dyer; Southern Illinois University Carbondale, Carbondale, IL Online Analysis of Metal-Binding Peptides Using an Ion-Selective Membrane Probe Coupled to ESI-MS TOF; Juan Astorga-Wells ^{1,2} ; Thomas White³; Craig M. Whitehouse³; Thorleif Lavold²; Hans Jörnvall¹; ^I Karolinska Institutet, Stockholm, Sweden; ² Biomotif AB, Danderyd, Sweden; ³ Analytica of Branford, Branford, CT Selective Extraction and Fractionation of Peptides from Multi-Protein Digests Using Polymeric and Dendrimeric Reverse Micelles for MS Analysis; Andrea Gomez-Escudero; Malar Azagarsamy; Sankaran Thayumanavan; Richard W. Vachet; University of Massachusetts, Amherst, MA Structural Elucidation of Isocyanate-Peptide Adducts Using Tandem Mass Spectrometry; Justin M. Hettick; Tinashe B. Ruwona; Paul D. Siegel; NIOSH, Morgantown, WV Intrinsic Gas Phase Reactivity Trends of a, b and y Peptide Ions: Effects of Size and Shape.; Patrícia Verardi Abdelnur¹; Livia S Eberlin²; Marcos N Eberlin³; ¹ ThomSon-Unicamp, Campinas, Brazil; ² Purdue University, West Lafayette, IN; ³ ThomSon Lab	MP 518 MP 519 MP 520	Medicine, Bronx, NY REACTIVE METABOLITES, 517 - 535 High Throughput Screening GSH Adducts Using Hybrid Linear Ion Trap Systems Coupling with Fast Chromatography at Clinically Relevant Dose Concentration; Elliott Jones¹, Claire Bramwell-German¹; Hesham Ghobarah²; Hua-fen Liu¹, ¹Applied Biosystems, Foster City, CA; ²Applied Biosystems / MDS Sciex, Concord, ON An Analytical Strategy to Study in vivo Metabolism of Fipexide Using QqQ _{LIT} and QqTOF Capabilities; David Tonoli¹, Emmanuel Varesio¹, Hans H. Maurer²; Gerard Hopfgartner¹, ¹University of Geneva, Geneve, Switzerland; ²University of Saarland, Homburg, Germany MP Mediated Amine-Activation of Reduced Nimesulide: Identification of Metabolites by LC-MS; Min Yang; Mahendra Chordia; Fengping Li; Timothy L Macdonald; University of Virginia, Charlottesville, VA Improved Detection of Reactive Drug Metabolites with Bromine-Containing Glutathione Analog Using Mass Defect and Isotope Pattern Matching; André LeBlanc; Tze Chieh Shiao; René Roy; Lekha Sleno; UQAM, Montreal, Canada Inexpensive Stable Isotope Labelling Approaches Combined with Mass Spectrometry to Screen and Characterize Reactive Drug Metabolites; Klaus Klarskoy; Daniel Defoy; Witold Neugebauer; Ibrahim
MP 505 MP 506 MP 507 MP 508	Squibb, Wallingford, CT Optimized Condition to Capture Peptides (Bradykinin and Buccalin) for Efficient Fractionation of a Peptide/Protein Mixture; Ven Ney Wong; Gary R. Kinsel; Daniel Dyer; Southern Illinois University Carbondale, Carbondale, IL Online Analysis of Metal-Binding Peptides Using an Ion-Selective Membrane Probe Coupled to ESI-MS TOF; Juan Astorga-Wells ^{1,2} ; Thomas White³; Craig M. Whitehouse³; Thorleif Lavold²; Hans Jörnvall¹; ^I Karolinska Institutet, Stockholm, Sweden; ² Biomotif AB, Danderyd, Sweden; ³ Analytica of Branford, Branford, CT Selective Extraction and Fractionation of Peptides from Multi-Protein Digests Using Polymeric and Dendrimeric Reverse Micelles for MS Analysis; Andrea Gomez-Escudero; Malar Azagarsamy; Sankaran Thayumanavan; Richard W. Vachet; University of Massachusetts, Amherst, MA Structural Elucidation of Isocyanate-Peptide Adducts Using Tandem Mass Spectrometry; Justin M. Hettick; Tinashe B. Ruwona; Paul D. Siegel; NIOSH, Morgantown, WV Intrinsic Gas Phase Reactivity Trends of a, b and y Peptide Ions: Effects of Size and Shape.; Patrícia Verardi Abdelnur¹; Livia S Eberlin²; Marcos N Eberlin³; ¹ ThomSon-Unicamp, Campinas, Brazil; ² Purdue University, West Lafayette, IN; ³ ThomSon Lab UNICAMP, Campinas, Sp, BRAZIL	MP 518 MP 519 MP 520	Medicine, Bronx, NY REACTIVE METABOLITES, 517 - 535 High Throughput Screening GSH Adducts Using Hybrid Linear Ion Trap Systems Coupling with Fast Chromatography at Clinically Relevant Dose Concentration; Elliott Jones¹; Claire Bramwell-German¹; Hesham Ghobarah²; Hua-fen Liu¹; ¹Applied Biosystems, Foster City, CA; ²Applied Biosystems / MDS Sciex, Concord, ON An Analytical Strategy to Study in vivo Metabolism of Fipexide Using QqQ _{LIT} and QqTOF Capabilities; David Tonoli¹; Emmanuel Varesio¹; Hans H. Maurer²; Gerard Hopfgartner¹; ¹University of Geneva, Geneve, Switzerland; ²University of Saarland, Homburg, Germany MP Mediated Amine-Activation of Reduced Nimesulide: Identification of Metabolites by LC-MS; Min Yang; Mahendra Chordia; Fengping Li; Timothy L Macdonald; University of Virginia, Charlottesville, VA Improved Detection of Reactive Drug Metabolites with Bromine-Containing Glutathione Analog Using Mass Defect and Isotope Pattern Matching; André LeBlanc; Tze Chieh Shiao; René Roy; Lekha Sleno; UQAM, Montreal, Canada Inexpensive Stable Isotope Labelling Approaches Combined with Mass Spectrometry to Screen and Characterize Reactive Drug Metabolites; Klaus Klarskov; Daniel Defoy; Witold Neugebauer; Ibrahim Hasibu; University de Sherbrooke, Sherbrooke, Canada
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MP 505 MP 506 MP 507 MP 508	Squibb, Wallingford, CT Optimized Condition to Capture Peptides (Bradykinin and Buccalin) for Efficient Fractionation of a Peptide/Protein Mixture; Ven Ney Wong; Gary R. Kinsel; Daniel Dyer; Southern Illinois University Carbondale, Carbondale, IL Online Analysis of Metal-Binding Peptides Using an Ion-Selective Membrane Probe Coupled to ESI-MS TOF; Juan Astorga-Wells ^{1,2} ; Thomas White³; Craig M. Whitehouse³; Thorleif Lavold²; Hans Jörnvall¹; ^I Karolinska Institutet, Stockholm, Sweden; ² Biomotif AB, Danderyd, Sweden; ³ Analytica of Branford, Branford, CT Selective Extraction and Fractionation of Peptides from Multi-Protein Digests Using Polymeric and Dendrimeric Reverse Micelles for MS Analysis; Andrea Gomez-Escudero; Malar Azagarsamy; Sankaran Thayumanavan; Richard W. Vachet; University of Massachusetts, Amherst, MA Structural Elucidation of Isocyanate-Peptide Adducts Using Tandem Mass Spectrometry; Justin M. Hettick; Tinashe B. Ruwona; Paul D. Siegel; NIOSH, Morgantown, WV Intrinsic Gas Phase Reactivity Trends of a, b and y Peptide Ions: Effects of Size and Shape.; Patrícia Verardi Abdelnur¹; Livia S Eberlin²; Marcos N Eberlin³; ¹ ThomSon-Unicamp, Campinas, Brazil; ² Purdue University, West Lafayette, IN; ³ ThomSon Lab UNICAMP, Campinas, Sp, BRAZIL	MP 518 MP 519 MP 520	Medicine, Bronx, NY REACTIVE METABOLITES, 517 - 535 High Throughput Screening GSH Adducts Using Hybrid Linear Ion Trap Systems Coupling with Fast Chromatography at Clinically Relevant Dose Concentration; Elliott Jones¹; Claire Bramwell-German¹; Hesham Ghobarah²; Hua-fen Liu¹; ¹Applied Biosystems, Foster City, CA; ²Applied Biosystems / MDS Sciex, Concord, ON An Analytical Strategy to Study in vivo Metabolism of Fipexide Using QqQ _{LIT} and QqTOF Capabilities; David Tonoli¹; Emmanuel Varesio¹; Hans H. Maurer²; Gerard Hopfgartner¹; ¹University of Geneva, Geneve, Switzerland; ²University of Saarland, Homburg, Germany MP Mediated Amine-Activation of Reduced Nimesulide: Identification of Metabolites by LC-MS; Min Yang; Mahendra Chordia; Fengping Li; Timothy L Macdonald; University of Virginia, Charlottesville, VA Improved Detection of Reactive Drug Metabolites with Bromine-Containing Glutathione Analog Using Mass Defect and Isotope Pattern Matching; André LeBlanc; Tze Chieh Shiao; René Roy; Lekha Sleno; UQAM, Montreal, Canada Inexpensive Stable Isotope Labelling Approaches Combined with Mass Spectrometry to Screen and Characterize Reactive Drug Metabolites; Klaus Klarskov; Daniel Defoy; Witold Neugebauer; Ibrahim Hasibu; University de Sherbrooke, Sherbrooke, Canada

- Anne Baumann; Wiebke Lohmann; Björn Meermann; Uwe Karst; *University of Münster, Münster, Germany*
- MP 523 Advantages in Utilizing Smaller Thiols to Trap Reactive Intermediates and Elucidate the Site(s) of Adduct Formation; Wing W Lam; Johnson and Johnson Pharmaceutical Research and De, Raritan, NJ
- MP 524 Simultaneous Detection and Quantitation of Iminium Ions by Hyphenated LC with Radioactivity Detector and Mass Spectrometry; R. F. Xu; J. Silva; H. K. Lim; J&J PRD, DMPK, Raritan, NJ
- MP 525 Trapping and Detecting Reactive Cyanide Intermediates without Toxic KCN Addition Using UPLC/QToF MSE; Don Laudicina; Liping Jin; Ajay Madan; Kayvon Jalali; Neurocrine Biosciences, San Diego, CA
- MP 526 Monitoring the Biodistribution and Bioactivity of
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 Qiyu Qiu; Anne-Laure Larroque; Marcos DiFalco; Line
 Roy; Bertrand J. Jean-Claude; Bernard F. Gibbs; McGill
 University, Montreal, Canada
- MP 527 Elucidation of a Novel Bioactivation Pathway of 3,4-Unsubstituted Isoxazole by Mass Spectrometry; Jian Yu; Maria Ribadeneira; Astrazenaca, Wilmington, DE
- MP 528 The Alternate Metabolism of Abacavir and its Role in Immune-Mediated Hypersensitivity Reactions in HIV Infected Individuals; Jeremy Netto^{1,3}; Niamh Keane^{2,3}; Ian Mullaney³; David Nolan^{2,3}; Simon Mallal^{2,3}; Robert Trengove^{1,3}; ¹Separation Science and Metabolomics Laboratory, Perth, Australia; ²Royal Perth Hospital, Perth, Australia; ³Murdoch University, Perth, Australia
- MP 529 Reactive Metabolite Trapping and Metabolite Identification Using Multiple Reagents and Specific Survey Scans on a Rapid Scanning Linear Ion Trap; James A. Ferguson¹; Stanley Rosenberg¹; Jenny Moshin¹; LaHoma Easterwood²; Sai Y. Chang³; ¹Applied Biosystems, Framingham, MA; ²CellzDirect, Austin, TX; ³MSMS Science LLC, Sedona, AZ
- MP 530 Analysis of Glutathione and Cysteinylglycine Conjugates of (+/-)-anti-7,8-dihydroxy-9,10-epoxy-7,8,9,10-tetrahydro-B[a]P by Liquid Chromatography/ Tandem Mass Spectrometry; Dipti Mangal^{1,2}; Clementina Mesaros^{1,2}; Trevor M. Penning^{1,2}; Ian A. Blair^{1,2}; **\frac{l}{center For Cancer Pharmacolo}, Philadelphia, PA; *\frac{2}{Centers of Excellence in Environmental Toxicology, Philadelphia, PA
- MP 531 Synthesis, Characterization and Identification of Cysteinyl Adduct of 15-Oxo Eicosatetraenoic Acid in Smoker's Urine; Jasbir S Arora; Ian A. Blair; University of Pennsylvania, Philadelphia, PA
- MP 532 A Novel Differential Analysis Algorithm for Low/High Resolution LC/MS Data: Applied to the Detection of Drug Metabolites and GSH-trapped Adducts; Marco Ruijken; MsMetrix, Maarssen, Netherlands
- MP 533 Profiling of Glutathione Conjugates of Electrophilic Metabolites in Plant Responses to Stress Using LC/TOF and Multiplexed CID; Xiaoli Gao; Abraham J. K. Koo; Jiangyin Bao; Gregg A. Howe; A. Daniel Jones; Michigan State Unviersity, East Lansing, MI
- MP 534 Novel AccQ•Tag UPLC/MS Method for High-Throughput Analysis of Amino Acids and Glutathione in Normal and HME-Transformed Human Mammary Epithelial Cell; <u>Diego F. Cortes</u>¹; Jenny M. Armenta¹; Suzy Torty²; Steven Akman²; Vladimir Shulaev¹; ¹Virginia Bioinformatics Institute,

- Blacksburg, VA; ²Wake Forest Universty, Winston-Salem. NC
- MP 535 Metabolism and Export of Lipid Peroxidation
 Products as Assayed in Human Monocytic THP-1
 Cells Using Electrospray LC-MS/MS; Brandi L.
 Langsdorf; Cristobal Miranda; Heather Kuiper; Ralph
 Reed; Fred Stevens; Oregon State University, Corvallis,
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 Enabling Generation and Recording of Unique
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 Changtong Hao²; Chris Lock¹; Alexandre Loboda¹; Min
 J. Yang¹; K W Michael Siu²; Bruce Thomson¹; ¹MDS
 Analytical Technologies, Concord, On, Canada; ²York
 University, Toronto, ON
- MP 537 An in vitro Investigation of the Reduction Potential of a Benzothiophene Sulfoxide Metabolite in Liver Microsomes, Cytosol, and Hepatocytes; Robert M.

 Iannucci; Carlo Sensenhauser; Shannon Dallas; Waqas Alam; Anthony Streeter; Kao Mark; Jose Silva; Hengkeang Lim; Johnson and Johnson PRD, Raritan, NJ
- MP 538 **Formula Determination and Relative Quantitation from Overlapping Ion Signals;** <u>Yongdong Wang;</u> Ming Gu; *Cerno Bioscience, Danbury, CT*
- MP 539 **Proteomic Investigation of Microbial Transformation of a Roxarsone, a Chicken Feed Additive.**; <u>Partha</u>

 <u>Basu</u>¹; Vadiraja Bhat²; Peter Chovanec¹; Stolz John¹; *Duquesne University, Pittsburgh, PA*; ²Agilent

 Technologies, Wilmington, DE
- MP 540 Statistical Differentiation of Xenobiotic Metabolism between Fresh and Cryo-Preserved Hepatocytes Using LC-MS-MS/MS Data from Fast Efficient Tandem Hybrid Instrumentation; Johnie Brown¹; Jeffrey Miller¹; James A. Ferguson¹; James Hill²; ¹Applied Biosystems, Framingham, MA; ²CellzDirect, Austin. TX
- MP 541 Metabolism of No-Methylserotonin, a Serotonergic Constituent from Black Cohosh, in Human Liver Microsomes and Intestinal Caco-2 cells; Dejan Nikolic; Soyoun Ahn; Jinghu Li; Richard B. van Breemen; University of Illinois College of Pharmacy, Chicago, IL
- MP 542 Investigation of Lycopene Metabolism and Degradation Products by LC-MS-MS and Stable Isotope Labeling; Jeff Dahl¹; Richard B. Van Breemen²; ¹Jeff Dahl, Chicago, IL; ²University of Illinois, Chicago, IL
- MP 543 Characterization of *in vitro* Metabolites of Troleandomycin, a Metabolism-Dependent Inhibitor of CYP3A4, by UPLC™ QTOF Mass Spectrometry; Joanna Barbara; Phyllis Yerino; David Buckley; Mark Horrigan; Paul Toren; Andrew Parkinson; *XenoTech*, *Lenexa*, KS
- MP 544 Combining Electrochemistry with LC/MS EC/LC/MS a Powerful Analytical Technique; Jean-pierre Chervet¹; Martin Eysberg¹; Uwe Karst²; ¹Antec Leyden BV, Zoeterwoude, Netherlands; ²University of Münster, Münster, Germany
- MP 545 Ultra-Trace Metabolite Identification Using UPLC/FTMS Combined With Chip-Based Nano-LC Separations.; Jesse L. Balcer; Jeffrey R. Gilbert; David G. Mccaskill; Gerrit J. Deboer; Brian M. Wendelberg; Dow AgroSciences, Indianapolis, IN
- MP 546 Characterization of the P450-Isozyme(s) Responsible For the Formation of 5-OH-CP-448,187 and N-oxide-

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	HPLC/ESI/MS/MS; Amin M. Kamel ¹ ; Wendy Wang ¹ ;		USA, Inc., Peabody, MA
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	Wang ¹ ; Amin M. Kamel ¹ ; ¹ Pfizer, Inc., Groton, CT;		Vegetables; Philip L. Wylie; Chin-kai Meng; Agilent
	² Pfizer, Groton, CT		Technologies, Wilmington, DE
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	by HPLC/RAM/ESI/MS/MS; Wendy Wang ¹ ; Kevin		
			Scott Niemann ¹ ; Spencer S. Walse ² , ^T CSS Analytical
	Colizza ² ; Amin M. Kamel ¹ ; ¹ Pfizer, Inc., Groton, CT;		Company, Inc., Shawnee, KS; ² United States Department
	² Pfizer, Groton, CT		of Agriculture-Agricultur, Parlier, CA
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MP 549	The Detection of Veterinary Residues in Meat Using		of Quality Determining Compounds in Wine without
1411 5 15	LC/MS/MS Analysis.; Stephen J. Lock ¹ ; Donna Potts ¹ ;		Sample Preparation; Stefanie Wirtz ¹ ; Volker Heidger ¹ ;
	Francisco Mocholi ² ; ¹ Applied Biosystems, Warrington,		Juergen Wendt ² ; ¹ Institut Heidger, Kesten, Germany;
	Transisco Mocilon, Applied Blosystems, Warrington,		² Agilent Technologies, Waldbronn, Germany
1 CD 550	UK; ² SAILab, Barcelona, Spain	MP 563	Fast Analysis of Flonicamid and Its Metabolites in
MP 550	Screening of Agrochemicals in Foodstuffs and Water	WII 303	Agricultural Foods by RPLC-MS/MS; Andre
	Using Low Temperature Plasma (LTP) Ambient		Agricultural roots by KrLC-M5/M5, Allele
	Mass Spectrometry; <u>Joshua S Wiley</u> ¹ ; Juan F Garcia-		Szczesniewski ¹ ; Elizabeth Culbert ² ; Richard Barry ¹ ;
	Reyes ^{1,2} ; Jason Harper ¹ ; Nicholas Charipar ¹ ; Zheng		Vince Herbert ² ; Matt Hengel ³ ; ¹ Agilent Technologies,
	Ouyang ¹ ; R. Graham Cooks ¹ ; ¹ Purdue University, West		Santa Clara, CA; ² Washington State University-Tri-
	Lafayette, IN; ² University of Jaen, Jaen, Spain		Cities, Richland, WA; ³ University of California at Davis,
MP 551	High-Performance Liquid Chromatography		Davis, CA
WII 331	Electrospray Ionization Fourier Transform Ion	MP 564	Simultaneous Analysis of 14 Mycotoxins, and 150
			Pesticides in Crude Extracts of Grains by
	Cyclotron Resonance Mass Spectrometry of Citrus		LC/MS/MS; Juergen Kunze ² ; Andrea Voller ² ; Hermann
	Extracts: Characterization and Comparisons; Mark R		Schmalstieg ² ; Ingrid Bujara ² ; Kristin Von Czapiewski ¹ ;
	Crosswhite; Florida State University, Tallahassee, FL		Birgit Schlutt ¹ ; Andre Schreiber ³ , ¹ Applied Biosystems
MP 552	MALDI-TOF/TOF Analysis of Sugar Beet Pectin-		blight Schiutt, Alidie Schieloet, Applied Biosystems
	Protein Complex; Alberto Nuñez; Marshall L. Fishman;		part of Life Technologies, Darmstadt, Germany; ² SGS,
	Laurie Fortis; Hoa K. Chau; USDA-ARS-ERRC,	_	Hamburg, Germany; ³ Applied Biosystems, Concord, ON
	Wyndmoor, PA		MALDI SAMPLE PREPARATION, 565 - 583
MP 553		MP 565	MALDI SAMPLE PREPARATION, 565 - 583
MP 553	A MALDI Gel Imaging Approach to Improve 2DE	MP 565	MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing
MP 553	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool	MP 565	MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High
MP 553	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; Dr. Santanu Deb-choudhury; S.	MP 565	MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF
MP 553	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; <u>Dr. Santanu Deb-choudhury</u> ; S. Clerens; J. E. Plowman; K. Y. Yong; C. D. Cornellison;	MP 565	MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF MS.; Stephen J. Hattan; Marvin Vestal; Virgin
MP 553	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; Dr. Santanu Deb-choudhury; S. Clerens; J. E. Plowman; K. Y. Yong; C. D. Cornellison; A. J. Hancock; H. Koehn; A. Thomas; J. M. Dyer;		MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF MS.; Stephen J. Hattan; Marvin Vestal; Virgin Instruments Corporation, Sudbury, MA
	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; Dr. Santanu Deb-choudhury; S. Clerens; J. E. Plowman; K. Y. Yong; C. D. Cornellison; A. J. Hancock; H. Koehn; A. Thomas; J. M. Dyer; AgResearch Limited, Christchurch, New Zealand	MP 565	MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF MS.; Stephen J. Hattan; Marvin Vestal; Virgin Instruments Corporation, Sudbury, MA Is Liquid UV-MALDI a Real Alternative to Solid
MP 553	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; Dr. Santanu Deb-choudhury; S. Clerens; J. E. Plowman; K. Y. Yong; C. D. Cornellison; A. J. Hancock; H. Koehn; A. Thomas; J. M. Dyer; AgResearch Limited, Christchurch, New Zealand Mass Spectrometry Identification of Plant Host		MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF MS.; Stephen J. Hattan; Marvin Vestal; Virgin Instruments Corporation, Sudbury, MA Is Liquid UV-MALDI a Real Alternative to Solid State UV-MALDI? Mark W Towers; Kieran Rollin; Ali
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	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; Dr. Santanu Deb-choudhury; S. Clerens; J. E. Plowman; K. Y. Yong; C. D. Cornellison; A. J. Hancock; H. Koehn; A. Thomas; J. M. Dyer; AgResearch Limited, Christchurch, New Zealand Mass Spectrometry Identification of Plant Host Proteins that Interact with Secreted Bean Rust Pathogen Proteins; Ruiqiang Chen ^{1,2} ; Mark L. Tucker ¹ ;	MP 566	MALDI SAMPLE PREPARATION, 565 - 583 Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF MS.; Stephen J. Hattan; Marvin Vestal; Virgin Instruments Corporation, Sudbury, MA Is Liquid UV-MALDI a Real Alternative to Solid State UV-MALDI? Mark W Towers; Kieran Rollin; Ali Tiss; Rainer Cramer; University of Reading, Reading, UK
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MP 554	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; Dr. Santanu Deb-choudhury; S. Clerens; J. E. Plowman; K. Y. Yong; C. D. Cornellison; A. J. Hancock; H. Koehn; A. Thomas; J. M. Dyer; AgResearch Limited, Christchurch, New Zealand Mass Spectrometry Identification of Plant Host Proteins that Interact with Secreted Bean Rust Pathogen Proteins; Ruiqiang Chen 1,2; Mark L. Tucker 1; Caren Chang 2; Bret Cooper 1, 1 USDA-ARS, Beltsville, MD; 2CBMG, University of Maryland, College Park, MD	MP 566	Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF MS.; Stephen J. Hattan; Marvin Vestal; Virgin Instruments Corporation, Sudbury, MA Is Liquid UV-MALDI a Real Alternative to Solid State UV-MALDI? Mark W Towers; Kieran Rollin; Ali Tiss; Rainer Cramer; University of Reading, Reading, UK High Sensitivity α-cyano-4-Chlorocinnamic Acid Liquid Matrices for UV-MALDI MS; Mark W Towers; Rainer Cramer; The University of Reading,
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MP 554 MP 555 MP 556	A MALDI Gel Imaging Approach to Improve 2DE Spatial Representation of Highly Homologous Wool Keratin Proteins; Dr. Santanu Deb-choudhury; S. Clerens; J. E. Plowman; K. Y. Yong; C. D. Cornellison; A. J. Hancock; H. Koehn; A. Thomas; J. M. Dyer; AgResearch Limited, Christchurch, New Zealand Mass Spectrometry Identification of Plant Host Proteins that Interact with Secreted Bean Rust Pathogen Proteins; Ruiqiang Chen ^{1,2} ; Mark L. Tucker ¹ ; Caren Chang ² ; Bret Cooper ¹ ; JUSDA-ARS, Beltsville, MD; CBMG, University of Maryland, College Park, MD Determination of Coccidiostats in Feed and Animal Produce by LC-MS; Pavel Metalnikov; Olga Nasyrova; Boris Krapivkin; Alexander Komarov; Alexander Panin; The All-Russia State Centre for Quality and Standa, Moscow, Russian Federation Solid Phase Extraction Combined with Liquid Chromatography—Mass Spectrometry for Pharmacokinetics Study of Enrofloxacin and Metabolites in Fish.; Wei-Hsun Wang ¹ ; Tzung-Jie Yang ¹ ; Chi-Chung Chou ¹ ; Shao-Kuang Chang ² ; Maw-Rong Lee ¹ ; National Chung Hsing University, Taichung, Taiwan; National Taiwan University, Taipei, Taiwan Rapid Trace Analysis of Chloramphenicol in Honey Using Molecularly Imprinted Polymer(MIP) LDTD- APCI-MS/MS; Grégory Blachon ¹ ; Pierre Picard ² ; E. Real Paquin ¹ ; Université Laval, Québec, Canada; Phytronix Technologies, Inc., Quebec, QC	MP 566 MP 567 MP 568 MP 569	Three Dimensional MALDI Plates Employing Collimated-Hole Structures used to Coupling High Capacity, High Flow Separations to MALDI-TOF MS.; Stephen J. Hattan; Marvin Vestal; Virgin Instruments Corporation, Sudbury, MA Is Liquid UV-MALDI a Real Alternative to Solid State UV-MALDI? Mark W Towers; Kieran Rollin; Ali Tiss; Rainer Cramer; University of Reading, Reading, UK High Sensitivity α-cyano-4-Chlorocinnamic Acid Liquid Matrices for UV-MALDI MS; Mark W Towers; Rainer Cramer; The University of Reading, Reading, UK Concentration and in-situ Detection of Peptides Using MALDI Ionic Liquid Matrices; Siao-huei Yang; Cing-Hong Cai; Yen-Peng Ho; National Dong Hwa University, Hualien, Taiwan High Versatility and Quantitative Capability at Femtomol Level of the Liquid Matrix 3- Aminoquinoline/CHCA in MALDI Mass Spectrometry; Yuko Fukuyama; Kaoru Kaneshiro; Kenichi Taniguchi; Sadanori Sekiya; Shinichi Iwamoto; Koichi Tanaka; Shimadzu Corporation, Kyoto, Japan Alternative CHCA-Based Matrices for the Low Molecular Weight Compounds Analysis by UV- MALDI-MS; Tiffany Porta; Chantal Grivet; Emmanuel Varesio; Gerard Hopfgartner; School of Pharmaceutical Sciences, Geneva, Switzerland New 3D MALDI Plates Composed of Layered, Photo- Etched, Stainless Steel, Sheets.; Joe Fitzpatrick;

- MP 572 **LC-NALDI: Using Matrix-Free Nanostructured Targets for Peptide Fractionation and Analysis**;

 <u>Sergei Dikler</u>; Paul Kowalski; *Bruker Daltonics Inc.*, *Billerica, MA*
- MP 573 Nanoparticle-Induced Fragmentation for Structure Determination of Carbohydrates by MALDI-TOF

 MS; Rofe-Amor Obena²; Mei-chun Tseng¹; Ying-Wei
 Lu³; Po-Chiao Lin³; Chun-Cheng Lin³; Yu-Ju Chen¹;

 Institute of Chemistry, Academia Sinica, Taipei,
 Taiwan; ²University of the Philippines-Diliman, Quezon
 City, Philippines; ³National Tsing Hua University,
 Hsinchu, Taiwan
- MP 574 Inhibitor Encapsulated Nanoparticles for Rapid Fucosidase Identification and Binding-Eptiopes Mapping; Han-Tsung Huang²; Mei-Chun Tseng²; Wei Hsu^{1,2}; Po-Chiao Lin²; Ching-Wen Ho⁴; Chun-Cheng Lin³; Chun-Hung Lin⁴; Yu-Ju Chen²; ¹Department of Chemistry, NCU, Taoyuan, Taiwan; ²Institute of Chemistry, Academia Sinica, Taipei, Taiwan; ³Institute of Chemistry, NTHU, Hsinchu, Taiwan; ⁴IBC, Academia Sinica, Taipei, Taiwan
- MP 575 Study of Surface-Assisted Laser
 Desorption/Ionization Mass Spectrometry using
 Metal Sulfide Particles as a Matrix; Akemi Ryoda;
 Tsuyoshi Yoshioka; Shuji Kagawa; Mitsubishi Chemical
 Group, Science & Technology, Yokohama, Japan
- MP 576 Electric Field Enhanced MALDI Sample Preparation via Induction Based Fluidics; <u>Drew Sauter</u>; Nanoliter, LLC, Henderson, NV
- MP 577 The Design and Preparation of an Adequate Sample Cell Suitable for Solvent-free Multi-Sample MALDI Analysis.; John Sami Maarouf; Alexandru Cernat; Calvin A. Austin; Sarah Trimpin; Wayne State University, Detroit, MI
- MP 578 Solvent-Free MALDI Analysis Avoids Sample Loss and in vitro Oxidation of Peptides and Lipids; Ellen D. Inutan; Thushani N. Herath; Sarah Trimpin; Wayne State University, Detroit, MI
- MP 579 Optimization of a Modified Aerospray Deposition Device for the Preparation of Samples for Quantitative Analysis by MALDI TOFMS; April Holcomb; Kevin G. Owens; Drexel University, Philadelphia, PA
- MP 580 On-Line Nano Aerosol Sample Deposition for MALDI Mass Spectrometry; Yuqian Gao; Murray V. Johnston; University of Delaware, Newark, DE
- MP 581 An Improved Calibrant System for MALDI-TOF MS
 Characterization of Peptides, Proteins, and Synthetic
 Polymers; Scott M. Grayson; Tulane University, New
 Orleans, LA
- MP 582 Reverse Thin Layer Method for Enhanced Ion Yields of Oligosaccharides in Matrix-Assisted Laser Desorption/Ionization; Takashi Nishikaze; Junko Amano; The Noguchi Institute, Itabashi, JAPAN
- MP 583 Investigating MALDI Signal Enhancement of Peptides after Selective Extraction by Polymeric Reverse Micelles; Nadnudda Rodthongkum; Yangbin Chen; Sankaran Thayumanavan; Richard Vachet; University of Massachusett, Amherst, MA

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MP 584 MALDI-MSn Quantitation by Selective Isolation of Analyte and Internal Standard Ions Using a Multi-Notch SWIFT Waveform; Richard F. Reich; Kyle N. Cromwell; Richard A. Yost; University of Florida, Gainesville, FL

- MP 585 Tandem Mass Spectrometry and High Resolution/Accurate Mass Analysis of Metal-Cluster Ions of Pigments from Painted Works of Art; Michael P. Napolitano¹; Ping-Chung Kuo²; Julie Arslanoglu³; Richard A. Yost¹; ¹University of Florida, Gainesville, FL; ²National Formosa University, Yunlin, Taiwan; ³The Metropolitan Museum of Art, New York, NY
- MP 586 MALDI-DITMS/MS for High Mass, High Sensitivity and High Resolution Measurement; Koichi Tanaka; Sadanori Sekiya; Shinichi Iwamoto; Shimadzu Corporation, Kyoto, Japan
- MP 587 The Solvent-Matrix Effect of Lipidomics Using an array Plate for MALDI-QIT-TOF-MS; Evelyn H.

 <u>Kim</u>¹; Yangsun Kim²; David M. Lubman¹; ¹University of Michigan, Ann Arbor, MI; ²Hudson Surface Technology, Newark, NJ
- MP 588 LC-MALDI with an Ion Trap Orbitrap Hybrid Instrumentation: Decoupled Method Setup; Kerstin Strupat¹; Huy Bui²; Rosa Viner²; Justin Blethrow²; Yue Xuan¹; Viatcheslav V. Kovtoun²; George Stafford²;

 ¹Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany; ²Thermo Fisher Scientific, San Jose, CA
- MP 589 Studying Multiple Cupperated Peptides Using MALDI-TOF Mass Spectrometry; Zhaoxiang Wu; David H. Russell; Texas A&M University, College Station, TX
- MP 590 Laser Desorption/Tandem Mass Spectrometry of Doubly Cationized, Singly Charged Ions Found in Painted Works of Art; Ping-Chung Kuo¹; Michael P. Napolitano²; Vivian E. Cornélio³; Julie Arslanoglu⁴; Richard A. Yost²; ¹National Formosa University, Yunlin, Taiwan; ²University of Florida, Gainesville, FL; ³Federal University of São Carlos, São Carlos, SP Brazil; ⁴The Metropolitan Museum of Art, New York, NY
- MP 591 Screening for Microbial Protein Over-Expression in Complex Matrix, Using MALDI-LTQ-Orbitrap;

 Thomas Moehring¹; Kerstin Strupat¹; Michiel Akeroyd²; Rob van der Hoeven²;

 Thermo Fisher Scientific,
 Bremen, Germany;

 DSM Food Specialties B.V, Delft,
 The Netherlands
- MP 592 Investigation into the Relationship between Proton Affinity and Small Drug-Like Molecule MALDI-QqQ Response; Kristin Geddes¹; Debra Mcloughlin¹; Richard King²; Emily Adarayan¹; ¹Merck and Co, Inc, West Point, PA; ²PharmaCadence Analytical, Quakertown, PA
- MP 593 Balancing the MRM Transition of Small Molecules, Substrate/Product Conversion for Enhances Label-Free Enzyme Inhibitor Screening; Rakesh Rathore¹; Jay Corr²; Kenneth D. Greis¹; ¹University of Cincinnati, Cincinnati, OH; ²MDS Analytical Technologies, Concord, ON

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- MP 594 Hemoglobin Analysis Using an LTQ-Orbitrap Top-Down Platform; Roger Theberge; Weiwei Tong; Giuseppe Infusini; Mark E. McComb; Catherine E. Costello; Boston University School of Medicine, Boston, MA
- MP 595 Deciphering Human Cardiac Troponin Modifications for Understanding and Diagnosis of Heart Failure: A Top-Down Mass Spectrometry-Based Disease Proteomics Approach; Jiang Zhang¹; Moltu Guy¹; Qingge Xu¹; M Shahriar Salamat¹; Ken H. Young¹; Jeffery W. Walker¹,²; Ying Ge¹; ¹University of Wisconsin-Madison, Madison, WI; ²University of Arizona, Tucson, AZ

- MP 596 Top-Down Protein Identification in Sera from Colorectal Cancer Patients Using 15 Tesla FTICR-MS; Simone Nicolardi¹; Yuri E.M. Van Der Burgt¹; Hans Dalebout¹; Wilma E. Mesker¹; Marco R. Bladergroen¹; Remco Swart²; Jens Fuchser³; Magnus Palmblad¹; Rob A. Tollenaar¹; André M. Deelder¹;

 ILeiden University Medical Ce, Leiden, Netherlands; **Dionex, Amsterdam, the Netherlands; **3Bruker Daltonik GmbH, Bremen, Germany
- MP 597 Mass Spectrometric Approaches to the Identification and Characterization of the Target Proteins of (R)-Lacosamide Drug; Onrapak Reamtong¹; Steven W. Cotten²; Pierre Morieux²; Ki Duk Park²; Rihe Liu²; Harold Kohn²; Claire Eyers¹; Simon J. Gaskell¹;

 ¹University of Manchester, Manchester, UK; ²UNC Eshelman, Chapel Hill, NC
- MP 598 A Widely Applicable Methodology for Quantitative Analysis of Therapeutic Proteins in Human Plasma; Jean-Marie Schmitter¹; Fabien Xuereb¹; Stephane Chaignepain¹; Frederic Godde¹; Dominique Breilh¹; Marie-Claude Saux¹; Christof Lenz²; Matthias Glueckmann²; ¹University of Bordeaux, Bordeaux, France; ²Applied Biosystems, Darmstadt, Germany
- MP 599 Large-Scale Identification and Quantification of Differentially Expressed Proteins Responding to Cisplatin Treatment in A2780 & A2780CIS Ovarian Cancer Cells; Steve Nguyen; Michael Lund Nielsen; Chanchal Kumar; Matthias Mann; Max Planck Institute for Biochemistry, D Martinsried, Germany
- MP 600 Proteome Analysis of Superior Temporal Gyrus in Schizophrenics and Non-Human Primates Treated with Anti-Psychotics Demonstrate Disease and Drug Specific Changes; Nilesh Tannu¹; Shixin Sun²; Richard Pintal²; Steven E Arnold³; Scott E. Hemby¹; ¹Wake Forest University School of Medicine, Winston Salem, NC; ²Applied Biosystems, Framingham, MA; ³University of Pennsylvania School of Medicine, Philadelphia, PA
- MP 601 Using Stable Isotopes and Tandem MS to Study the Metabolism of CNS-Derived Apolipoprotein E Isoforms; Kristin R Wildsmith; Wendy C Sigurdson; Randall J Bateman; Washington University, St. Louis, MO
- MP 602 iTRAQ 8plex Analysis of a Membrane Enriched Sub-Proteome from Post-Mortem Brain in Schizophrenia and Control Subjects.; Jane A English¹; Bruno Manadas²; David R Cotter³; Michael J Dunn¹; ¹UCD Conway Institute, University College Dublin, Dublin, Ireland; ²Center for Neuroscience and Cell Biology, Cantanhede, Portugal; ³Royal College of Surgeons, Dublin, Ireland
- MP 603 Characterization of Proteins in Cerebrospinal Fluid of Patients with HIV-Associated Neurocognitive Disorder using iTRAQ and Mass Spectrometry;

 Dawn Chen¹; Caroline F Anderson¹; Robert J. Cotter²; Ned Sacktor¹; Justin McArthur¹; Avindra Nath¹;

 Department of Neurology, Johns Hopkins University, Baltimore, MD; ²Middle Atlantic MS Laboratory, Baltimore, MD
- MP 604 Proteomic Alterations in Response to in vitro
 Treatment with Velcade, Doxorubicin, and
 Dexamethasone in Multiple Myeloma Using 8-plex
 iTRAQ; Dominik Dytfeld²; Madhu Prasad²; Vadiraja B.
 Bhat³; Rong Zhao²; Alexey I. Nesvizhskii²; Andrzej J.
 Jakubowiak²; Arun Sreekumar¹; **Imedical College of Georgia, Augusta, GA; **2University of Michigan, Ann
 Arbor, MI; **3Agilent Technologies, Wilmington, DE

- MP 605 Relative Serum Protein Quantification Based upon ICPL and 2D-LC-MS Identifies Potential Frailty Biomarkers in Elderly Patients; Andrei Turtoi; Gabriel Mazzucchelli; Rowan L. Dobson; Edwin De Pauw; University of Liege, Liege, Belgium
- MP 606 Unambiguous Detection and Quantitation of Fulllength Thioredoxin (TRX) and Truncated Thioredoxin (TRX80) in Complex Samples by MALDI; Susan C Follstaedt¹; David R Graham¹; Keling Dong²; Marjorie S Minkoff²; M. Christine Zink¹; Christie L Hunter²; ¹Johns Hopkins, Baltimore, MD; ²Applied Biosystems, Foster City, CA
- MP 607 **Development of an srm-based apolipoprotein Panel**Assay; Amol Prakash³; Mingming Ning²; Taha Rezai⁴;
 Bryan Krastins¹; David Sarracino⁴; Michael Athanas⁵;

 Mary F Lopez¹; ¹ThermoFisher, Cambridge, MA;

 ²Massachusetts General Hospital, Harvard, Boston, MA;

 ³ThermoFisher Scientific, Cambridge, MA; ⁴Thermo
 Fisher Scientific, San Jose, CA; ⁵VAST Scientific,
 Wayland, MA
- MP 608 Development of Quantitative Mass Spectrometry
 Assays for Cellular Pathways: Elucidating Drug
 Resistance in Multiple Myeloma; Yun Xiang; Lori
 Hazlehurst; John Koomen; H. Lee Moffitt Cancer
 Center, Tampa, FL
- MP 609 Proteomic Workflow for Discovery of Serum Carrier Protein-Bound Biomarker Candidates of Alcohol Abuse Using Liquid Chromatography Tandem Mass Spectrometry; Heather N. Ringham; Xianyin Lai; David W. Crabb; Suthat Liangpunsakul; Frank Witzmann; Indiana University School of Medicine, Indianapolis, IN
- MP 610 Rapid Proteomics Approach for the Identification of Peptide Hydrazide Adducts by Atmospheric Pressure MALDI MS/MS; Seshu Gudlavalleti^{1,1}; Sudha Chennasamudram²; Jane Razumovskaya^{1,1}; Appavu Sundaram^{1,1}; Vladimir M. Doroshenko^{1,1}; Science and Engineering Serv, Columbia, MD; Center for Biologics Evaluation and Research (FDA), Bethesda, MD
- MP 611 Interest of a MALDI-FTICR Mass Spectrometry
 Approach for Identification of Protein Targets
 involved in Photodynamic Therapy; <u>David Da Silva</u>¹;
 Thierry Wasselin²; Benoît Maunit¹; Vincent Carre¹; Lina
 Bezdetnaya³; Jean Francois Muller¹; ¹LSMCL Université
 Paul Verlaine, Metz, France; ²LSMBO, Strasbourg,
 France; ³CRAN-CAV, Nancy, France
- MP 612 Sample Preparation and Instrumental Protocols for Improved Reflectron and LIFT Detection of Ions Up to 10 kDa; Christine Bunai¹; Julius Nyalwidhe²; Lisa H. Cazares³; Dennis Manos¹; William E. Cooke¹; Dariya Malyarenko¹; ¹College of William and Mary, Williamsburg, VA; ²Eastern Virginia Medical Sch, Norfolk, VA; ³Eastern Virginia Medical School, Norfolk, VA
- MP 613 Proteomic Analysis of FFPE Amyloid Plaques Using Laser Microdissection and Nano-Flow LC-MS/MS;

 Jason D Theis; Jeff D Gamez; Julie A Vrana; Karen L

 Grogg; Ahmet Dogan; Mayo Clinic, Rochester, MN
- MP 614 Mining the Archival Formalin-Fixed Proteome:

 Method Optimisation and Validation of an Efficient
 Label-Free Quantitative Shotgun Proteomic
 Strategy; Niroshini Nirmalan¹; Christopher Hughes²;
 Therese McKenna²; Jianhe Peng¹; James Langridge²;
 Patricia Harnden¹; Peter Selby¹; Rosamonde E. Banks¹;

 University of Leeds, Leeds, UK; **2Waters Corporation, Manchester, UK

- MP 615 Rapid Detection of Proteins in Complex Mixtures by Extractive Electrospray Ionization Mass Spectrometry; Shuiping Yang¹; Huanwen Chen^{1,2}; Jianqiang Li¹; Bin Hu¹; Xie Zhang¹; Yufen Zhou¹; Lili Zhang²; **Ieast China Institute of Technology, Fuzhou, P. R. China; **Ijlin University, Changchun, P. R. China
- MP 616 Development of a Breast Cancer Tissue Specific AMT Database: A New Tool for Biomarker Discovery; Arzu Umar¹; Heather M. Mottaz²; Samuel O. Purvine²; Anita M. Trapman-Jansen¹; Astrie Thakoursingh¹; Theo M. Luider³; John A. Foekens¹; Ljiljana Pasa-tolic²; **IErasmus MC, Medical Oncology, Rotterdam, Netherlands; **Pacific Northwest National Laboratory Battelle, Richland, WA; ***JErasmus MC, Neuro-oncology, Rotterdam, Netherlands
- MP 617 Approaching Solid Tumor Heterogeneity by Tissue Proteomics Using Laser Capture Microdissection and Biological Mass Spectrometry; Donald Johann¹; Jaime Rodriquez-Canales¹; Sumana Mukherjee¹; Darue A. Prieto²; Jeffrey Hanson¹; Michael Emmert-Buck¹; Timothy D. Veenstra³; Josip Blonder³; ¹NIH, Bethesda, MD; ²NIC-Frederick (SAIC), Frederick, MD; ³SAIC-Frederick, Inc., Frederick, MD
- MP 618 Statistical Significance in MS-Based Label-Free Protein Quantification Analysis Applied in Clinical Research; Daniel C. Chamrad¹; Barbara Sitek²; Sebastian Link²; Christian Stephan²; Katharina Podwojski²; Kai Stühler²; Martin Blueggel¹; Korte Birgit²; Helmut E. Meyer²; **Protagen AG, Dortmund, Germany; **2Ruhr-University Bochum, Dortmund, Germany
- MP 619 Optimized Two-Dimensional Chromatographic Methods for Peptide Biomarker Discovery and Validation in Clinical Samples; Keith Fadgen¹; Martha Stapels¹; Jim Langridge¹; J. Will Thompson²; Arthur Moseley²; ¹Waters Corporation, Milford, MA; ²Duke University School of Medicine, Durham, NC
- MP 620 Application of Peptide Library-Based Affinity-Chromatography to Analysis of Saliva Proteome;
 Zhiguo Zheng²; Nagarajan Chandramouli¹; Weimin Mao²; Zhiqiang Ling²; Qing Fang¹; Daniel Malamud³;
 Haiteng Deng¹,³, ¹The Rockefeller University, New York, NY; ²Zhejiang Cancer Research Institute, Hangzhou, China; ³New York University, New York, NY
- MP 621 Labeling of Plasma Glutathione and Ophthalmate from 2H-Enriched Body Water: A Noninvasive Probe of the Redox Status of the Liver; Rajan S.

 Kombu¹; Guofang Zhang¹; John J. Mieyal¹; Vernon E. Anderson¹; Joanne K. Kelleher²; Juan R. Sanabria¹; Henri Brunengraber¹, ¹Case Western Reserve University, Cleveland, OH; ²Massachusetts Institute of Technology, Cambridge, MA

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- MP 622 Ion Conformation Changes in the Ion Trap / Drift Cell Interface on the Microsecond Timescale; Gregg Schieffer¹; Qin Zhao¹; Derrick L. Morast¹; Ethan R. Badman²; R. Sam Houk¹; Iowa State University, Ames, IA; ²Hoffmann-La Roche Inc., Nutley, NJ
- MP 623 Discrimination of Steroidal Glycoside Isomers by Collisionally Activated Dissociation of Transition Metal Complexes; Xiaoji Cao; Zhejiang university of Technology, Hangzhou, China
- MP 624 The Thermochemical Studies of Protonated Amine-Crown Ether Complexes: Extension of the Kinetic Method.; Michael Zickus; Sara Koepke; Kevin Chong; Victor Ryzhov; Northern Illinois University, Dekalb, IL

- MP 625 Multi-Pass UV-Photodissociation Implemented on a Hybrid QqTOF Mass Spectrometer for LC Analysis; Changtong Hao¹; J.C. Yves Le Blanc²; Alexandre Loboda²; Bruce Thomson^{1,2}; K W Michael Siu¹; ¹CRMS, York University, Toronto, Canada; ²MDS Analytical Technologies, Concord, ON, Canada
- MP 626 Infrared Multiphoton Dissociation of DNA Anions and Cations in a Dual-Cell Linear Ion Trap; Suncerae Smith¹; Myles Gardner¹; James Madsen¹; Aaron Ledvina²; Jennifer Brodbelt¹, ¹University of Texas Austin, Austin, TX; ²UW Madison, Madison, WI
- MP 627 **UV Photodissociation of Carboxy-Modified Peptides**; Byoung Joon Ko¹; Jennifer Brodbelt²; ¹UT-Austin, Austin, TX, ²The University of Texas, Austin, TX
- MP 628 **Top-Down Protein Fragmentation by Infrared**Multiphoton Dissociation in a Dual Cell Linear Ion
 Trap; James Madsen¹; Myles Gardner¹; Suncerae
 Smith¹; Aaron Ledvina²; Jennifer Brodbelt¹; ¹University
 of Texas Austin, Austin, TX; ²UW Madison, Madison,
 WI
- MP 629 Mass-Analyzed-Threshold-Ionization: A Versatile Method for the stUdy of the Structure of Halogenated Aromatic Compounds and Noble Gas Clusters.; Jurgen Grotemeyer; Frank Witte; Christian-Albrechts-Univ, Kiel, Germany
- MP 630 **Protonated Tryptophan Radicals in the Gas Phase**; <u>Joshua A Gregersen</u>; Frantisek Turecek; *University of Washington, Seattle, WA*
- MP 631 Metastable Atom-Activated Dissociation (MAD) within a Quadrupole Ion Trap Mass Spectrometry (QIT-MS).; Shannon Cook; Glen Jackson; Ohio University, Athens, OH
- MP 632 Comparison of Metastable Atom-Activation
 Dissociation (MAD), ETD and CAD of Peptides and
 Modified Peptides; Carolyn M. Zimmermann¹;
 Shannon Cook¹; Glen Jackson¹; Ralf Hoffmann²; ¹Ohio
 University, Athens, OH; ²Universität Leipzig, Leipzig,
 Germany
- MP 633 Study by FTICRMS and SORI-CID, ECD and IRMP FTICRMSⁿ of Cluster Ions produced by Electrosprayed KBrO₃ Solutions; Frédéric Aubriet; LSMCL Université Paul Verlaine, Metz, France
- MP 634 Higher Efficiency Protein Tandem Mass
 Spectrometry Using Multiple Correlated Harmonic
 Excitation Fields- (multi-CHEF)-ECD-FTICR-MS; Normat Karabacak¹; Qi Wang¹; Michael Easterling²;
 Jeffrey Agar¹; Brandeis University, Waltham, MA;

 Bruker Daltonics, Inc., Billerica, MA
- MP 635 Investigation Into the use of Lys-N Combined with Electron Transfer Dissociation on a Quadrupole Time-of-Flight Mass Spectrometer for Peptide Sequencing; Jim Langridge¹; Jeff Brown²; Shabaz Mohammed³; Nadia Taouatas³; Iain D G Campuzano¹; Albert J.R. Heck³, ¹Waters Corporation, Manchester, UK; ²Waters Micromass MS Technologies, Manchester, UK; ³Utrecht University, Utrecht, Netherlands
- MP 636 Radio Frequency-Free Electromagnetostatic Cell for ECD, CID and Combined ECD/CID Mass Spectrometry; Valery Voinov^{1,2}; Joseph S Beckman¹; Max L. Deinzer¹; Douglas F. Barofsky¹; ¹OSU, Corvallis, OR; ²PIBOC, RAS, Vladivostok, Russia
- MP 637 Activated Ion ECD in Radio Frequency Ion Trap for Precise de novo Peptide Sequencing; Hiroyuki Satake; Akihito Kaneko; Naomi Manri; Atsumu Hirabayashi; Takeshi Sakamoto; Central Research Laboratory, Hitachi Ltd., Tokyo, Japan

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MP 638	Probing ECD Charge Reduced Ions Using ECD and		Dichlorophenol; Mahendra K. Trivedi ¹ ; Rama Mohan
	CID (ECD/ECD and ECD/CID); Daniel A Thomas;		R. Tallapragada ² ; ¹ Adjunct Scientist,M. G.
	Takashi Baba; Gary L. Glish; <i>University of North</i>		Vidyamandir's Pharmacy Col, Mumbai, India; ² Retired
	Carolina, Chapel Hill, NC		Professor,I.I.T.Bombay, Mumbai, India
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	Takashi Baba ¹ ; Gary L. Glish ¹ ; ¹ University of North		Butylated Hydroxytoulene Treated with External
	Carolina, Chapel Hill, NC; ² Agilent Technologies,		Energy; Shrikant A. Patil ¹ ; Rama Mohan R.
	Wilmington, DE		Tallapragada ² , ¹ Adjunct Scientist, MGV's Pharmacy
MP 640	Gas-Phase Ion-Electron Reactions and Vibrational		College, Nashik, Mumbai, India; ² Retired Professor-
WII 040	Activation of Electrosprayed Intact Proteins in		I.I.T.Bombay, Mumbai, India
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	Desmond Kaplan ² ; Richard Vachet ¹ ; ¹ University of		Acid Methyl Esters (FAME); Gail A Harkey ¹ ; Douglas
	Massachusetts, Amherst, MA; ² Bruker Daltonics, Inc.,		Cameron ² ; James Chang ¹ ; ¹ Thermo Fisher Scientific,
	Billerica, MA	100 654	Schaumburg, IL; ² Montana Tech, Butte, MT
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	Texas, Austin, TX	MP 655	Introducing a New Advanced Data Processing
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	A. Al-saad ¹ ; Mohamed Amr ¹ ; Nagwa Zahran ² ; Abdul-		Technology, Gaithersburg, MD; ² Topchiev Institute of
	Fattah Helal ² ; ¹ Qatar University, Doha, Qatar; ² Atomic	MD 650	Petrochemical Synthesis RAS, Moscow, Russia
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	Human Serum by Liquid Chromatography Coupled to ICP-MS, ESI-Q-TOF-MS and QIT-MS; Lidia		<u>Churley</u> ² ; Harry Prest ² ; Matthew S. Klee ⁴ ; Celso Blatt ³ ;
	Siemieniako ² ; Josephine Bunch ¹ ; Alan G. Cox ² ;		
	Cameron W. Mcleod ² ; ¹ University of Birmingham,		¹ Stanford University, Stanford, CA; ² Agilent Technologies, Santa Clara, CA; ³ Agilent Technologies
MP 647	Birmingham, UK; ² University of Sheffield, Sheffield, UK Chemical Speciation of Bismuth by Gas		Brazil, Sao Paulo, Brazil; ⁴ Agilent Technologies Office,
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	Shettigar ¹ ; Rama Mohan R. Tallapragada ² ; ¹ Adjunct		Structural Elucidation of Unknowns; O. David Sparkman; Matthew Curtis; Monika Kaur; Jianhua Ren;
	Scientist, MGV's Pharmacy College, Mumbai, India;		
		MP 662	Patrick R. Jones; University of the Pacific, Antioch, CA
MD 650	² Retired Professor - I.I.T.Bombay, Mumbai, India	WIP 002	Using Comprehensive Gas Chromatographic
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	Tallapragada ² ; ¹ Adjunct Scientist,MGV's Pharmacy		
			David Sparkman ¹ ; ¹ University of the Pacific, Antioch,
	College, Mumbai, India; ² Retired Professor-		CA; ² NIST, Gaithersburg, MD; ³ Chemical Research
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	2,0-машиорупшис, 4- менюхурнены ани 2,4-		Detect Sulfonic Acid Esters in Mesylate Salt Drug

- **Substances and Drug Products**; Alina Domin-Turza; Samantha Leidner; Esther Hwang; <u>Paul M. Bigwarfe Jr.</u>; *Hospira, Inc., Lake Forest, IL*
- MP 664 Sensitivity Comparison of Electron and Negative Chemical Ionizations for Derivatized Aldehydes;

 Josef Beranek; Alena Kubatova; University of North Dakota, Chemistry Department, Grand Forks, ND
- MP 665 A Sensitive and Specific Methodology for Furfural Determination in a Pharmaceutical Product Using Headspace GC/MS and GC/FID; Yieng-hau Han; Jennifer Jakubowski; Zhong Li; Qingxi Wang; Merck Co., West Point, PA
- MP 666 Applying Headspace Trap Technology to the GC/MS
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 D. Goodman; Adam J. Patkin; Andrew N. Tipler;
 PerkinElmer, Inc, Shelton, CT
- MP 667 Relative Area Quantitation of Natural Product Compounds Using GC/MS and Deconvolution Algorithms; Michelle Lee; Albert Robbat; Tufts University, Medford, MA
- MP 668 Mass Spectra of Polyethylene Glycols, Glycol Acids, and Derivatives by GC-MS; Yufang Zheng; Yuxue Liang; Edward White V; Stephen E. Stein; NIST, Gaithersburg, MD
- MP 669 Human Plasma Free 8-iso-PGF2α Quantified Using a Modified Immunoaffinity Isolation-Stable Isotope Labeled Internal Standard GC/NICI/MS Technique.; Xianghong Chen; Kevin Yarasheski; Washington University School of Medicine, Saint Louis, MO
- MP 670 Confident Unknown Identification of SVOC
 Compounds by Combining NIST Library Search
 with Elemental Composition Determination; Jianping
 Chen¹; O. David Sparkman²; Ming Gu³; ¹Connecticut
 State Department of Environmental, Windsor, CT;
 ²University of the Pacific, Antioch, CA; ³Cerno
 Bioscience, Yardley, PA
- MP 671 The Measurement of Native Compounds in a
 Candidate Urine Standard Reference Material (SRM
 3671 Smokers' Urine) by Gas Chromatography/Mass
 Spectrometry; Bruce A. Benner, Jr.; Lane C. Sander;
 NIST, Gaithersburg, MD
- MP 672 Using a Novel Heartcut Device for Multidimensional GC to Reveal Small Peaks Otherwise Obscured by Large Peaks in Mass Chromatograms; Andrew Tipler¹; William D. Goodman³; Adam J. Patkin²;

 PerkinElmer Inc., Trumbull, CT; PerkinElmer, Inc, Shelton, CT; PerkinElmer, Shelton, CT